

SEQUENCE LISTING

<110> AVENTIS PHARMA S.A.

<120> ESSENTIAL GENES FROM C. ALBICANS AND A METHOD FOR
SCREENING ANTIMYCOTIC SUBSTANCES USING SAID GENES

<130> 16655

<140> PCT/EP99/07378

<141> 1999-09-13

<150> EP98402255.8

<151> 1998-09-11

<160> 25

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Probe

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gaactagata atattgtgaa gcaggcagag aaattagtca gtgagggtgc tacgattatt 300
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<213> Candida albicans

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<221> CDS

<222> (1)..(2364)

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<221> gene

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Ile Ser Leu Ser Phe Asn Thr Asp Phe His Lys Ala Ser Glu Leu Asp	
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Asn Leu Lys Tyr Ser Ile Asn Tyr Ala Val Ile Thr Arg Asn Val Thr	
50 55 60	
gaa ttt atg aaa tca aat gag cat tta aat ttc aag tca tta gga aat	240
Glu Phe Met Lys Ser Asn Glu His Leu Asn Phe Lys Ser Leu Gly Asn	
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Ile Ala Gln Ala Ile Ser Asp Ile Gly Leu Asp Gln Ser Arg Gly Gly	
85 90 95	
gga tct att gtg gat gtg acg ata aaa agt ttg aaa tca gaa ata aga	336
Gly Ser Ile Val Asp Val Thr Ile Lys Ser Leu Lys Ser Glu Ile Arg	
100 105 110	
gct gaa agt gtc gaa tat aaa att aat aga aac act ttg ggt caa ccc	384
Ala Glu Ser Val Glu Tyr Lys Ile Asn Arg Asn Thr Leu Gly Gln Pro	
115 120 125	
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Val Pro Leu Asp Ile Phe Gln Val Asn Lys Leu Arg Leu Leu Thr Ile	
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ttc aaa gat atg gaa cca gtt aaa ttt gaa aac aca att gct caa act	768
Phe Lys Asp Met Glu Pro Val Lys Phe Glu Asn Thr Ile Ala Gln Thr	
245 250 255	
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Asn Arg Ala Phe Asn Leu Pro Val Glu Asn Glu Lys Thr Glu Asp Tyr	
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Thr Gly Tyr His Thr Ala Phe Ile Ala Phe Gly Ser Asn Thr Gly Asn	
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Gln Val Glu Asn Ile Thr Asn Ser Phe Glu Leu Leu Gln Lys Tyr Gly	
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atc acc ata gaa gca act tca tca ttg tac att tct aaa cca atg tat	960
Ile Thr Ile Glu Ala Thr Ser Ser Leu Tyr Ile Ser Lys Pro Met Tyr	
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Tyr Leu Asp Gln Pro Asp Phe Phe Asn Gly Val Ile Lys Val Asn Phe	
325 330 335	
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Gln Asn Ile Ser Pro Phe Gln Leu Leu Lys Ile Leu Lys Asp Ile Glu	
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Gln Pro Leu Cys Glu Val Leu Pro Pro Asp Tyr Ile His Pro Ile Ser	
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 145 150 155 160
 Asp Leu Gln Phe Lys Ile Glu Pro Asn Ser Asn Leu Tyr Phe His Gln
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 355 360 365
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 Ser Arg Leu Pro Val Lys Asp Asn Ile Leu Lys Phe Asp Gln Ile Asn
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 His Lys Ser Pro Thr Leu Ile Met Gly Ile Leu Asn Met Thr Pro Asp
 465 470 475 480
 Ser Phe Ser Asp Gly Gly Lys His Phe Gly Lys Glu Leu Asp Asn Thr
 485 490 495
 Val Lys Gln Ala Glu Lys Leu Val Ser Glu Gly Ala Thr Ile Ile Asp
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 Asp Ile Ser Met Gly Lys Tyr Asp Glu Lys Ile Phe Asp Val Val Ala
 580 585 590
 Lys Tyr Gly Cys Pro Tyr Ile Met Asn His Thr Arg Gly Ser Pro Lys
 595 600 605
 Thr Met Ser Lys Leu Thr Asn Tyr Glu Ser Asn Thr Asn Asp Asp Ile
 610 615 620
 Ile Glu Tyr Ile Ile Asp Pro Lys Leu Gly His Gln Glu Leu Asp Leu
 625 630 635 640
 Ser Pro Glu Ile Lys Asn Leu Leu Asn Gly Ile Ser Arg Glu Leu Ser
 645 650 655
 Leu Gln Met Phe Lys Ala Met Ala Lys Gly Val Lys Lys Trp Gln Ile
 660 665 670
 Ile Leu Asp Pro Gly Ile Gly Phe Ala Lys Asn Leu Asn Gln Asn Leu
 675 680 685
 Ala Val Ile Arg Asn Ala Ser Phe Phe Lys Lys Tyr Ser Ile Gln Ile
 690 695 700
 Asn Glu Arg Val Asp Asp Val Thr Ile Lys His Lys Tyr Leu Ser Phe
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Asn Gly Ala Cys Val Leu Val Gly Thr Ser Arg Lys Lys Phe Leu Gly
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Thr Leu Thr Gly Asn Glu Val Pro Leu Asp Arg Val Phe Gly Thr Gly
 740 745 750

Ala Thr Val Ser Ala Cys Ile Glu Gln Asn Thr Asp Ile Val Arg Val
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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Probe

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<212> DNA

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20 25 30	
aat aat cct tat gct aat tta agc act ggt gaa aaa agt agg agt cgc	144
Asn Asn Pro Tyr Ala Asn Leu Ser Thr Gly Glu Lys Ser Arg Ser Arg	
35 40 45	
cat aac act ggt agt tct tat gtt tct cca tat ggc ggc ggt aat gga	192
His Asn Thr Gly Ser Ser Tyr Val Ser Pro Tyr Gly Gly Gly Asn Gly	
50 55 60	
gag gag aat gct tat act ggg aat aac aac aaa tca aat act agt ggt	240
Glu Glu Asn Ala Tyr Thr Gly Asn Asn Asn Lys Ser Asn Thr Ser Gly	
65 70 75 80	
aat tta tta caa gtt cct gga gca gga gga gga gat ttg aat tct	288
Asn Leu Leu Gln Val Pro Gly Ala Gly Gly Gly Gly Asp Leu Asn Ser	
85 90 95	
aat aag aaa caa agt cga aga atg agt att cat gta tca gct cgt caa	336
Asn Lys Lys Gln Ser Arg Arg Met Ser Ile His Val Ser Ala Arg Gln	
100 105 110	
cat gga aga tca ttt tca caa act ggt cca att gat atg gca aat tta	384
His Gly Arg Ser Phe Ser Gln Thr Gly Pro Ile Asp Met Ala Asn Leu	
115 120 125	
ccg gca tta cct aaa ata ggt ggt gtt act act agt ggt gtt ggc ggt	432
Pro Ala Leu Pro Lys Ile Gly Gly Val Thr Thr Ser Gly Val Gly Gly	
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gct ggt ggt gat gtt atg aca agg act ggg gga ttg acg ata gaa caa	480
Ala Gly Gly Asp Val Met Thr Arg Thr Gly Gly Leu Thr Ile Glu Gln	
145 150 155 160	
aaa ata ttc aaa gaa tta agt caa gga tca gca gct gaa gtt gat gat	528
Lys Ile Phe Lys Glu Leu Ser Gln Gly Ser Ala Ala Glu Val Asp Asp	
165 170 175	
tat tac aag aca tta ttg aaa cag aaa aat tta atc act cgt gac att	576
Tyr Tyr Lys Thr Leu Leu Lys Gln Lys Asn Leu Ile Thr Arg Asp Ile	
180 185 190	
aag gat aat att aat cag aat caa aaa aat att tta caa tta aca aaa	624
Lys Asp Asn Ile Asn Gln Asn Gln Lys Asn Ile Leu Gln Leu Thr Lys	

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aaa gaa tta tat gaa gtt tta ggt tat ttc aaa gaa tca gct caa cgt			720
Lys Glu Leu Tyr Glu Val Leu Gly Tyr Phe Lys Glu Ser Ala Gln Arg			
225	230	235	240
aga tta gaa ttg gaa ttt gaa cca gaa aca caa aaa gaa ctt cat ctg			768
Arg Leu Glu Leu Glu Phe Glu Pro Glu Thr Gln Lys Glu Leu His Leu			
245	250		255
cct caa aaa agt aat caa ttg ggt att cct agt aat aaa aag aaa gat			816
Pro Gln Lys Ser Asn Gln Leu Gly Ile Pro Ser Asn Lys Lys Lys Asp			
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Arg Ser Ser Ile Met Val Leu Lys Lys Met Trp Asp Ser Gln Leu Gln			
275	280		285
tca tta ttt aaa cat gtt gac ggt gca tca aaa ttt gtc caa cca tta			912
Ser Leu Phe Lys His Val Asp Gly Ala Ser Lys Phe Val Gln Pro Leu			
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ccc aat aga cac att gtc gcg gaa agt gga cga tgg ttt gaa gtt aat			960
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gtg ggg aat tgg aaa cca agt tat cca act cat tta ttt ata ttt aat			1008
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355	360		365
gtt caa tgt tgg ccc tta act caa gta tca tta caa caa atc aaa tca			1152
Val Gln Cys Trp Pro Leu Thr Gln Val Ser Leu Gln Gln Ile Lys Ser			
370	375		380
ccg aaa aaa gat gac gat aag atg tat ttt atc aat ctt aaa tcc aaa			1200
Pro Lys Lys Asp Asp Asp Lys Met Tyr Phe Ile Asn Leu Lys Ser Lys			
385	390	395	400
tct tta agt tat gta tac ctg acg gat cgt tat gat cat ttt gtg aaa			1248
Ser Leu Ser Tyr Val Tyr Leu Thr Asp Arg Tyr Asp His Phe Val Lys			
405	410		415
gtt acg gaa gca ttt aat aaa ggt aga aat gaa atg att caa agt gaa			1296
Val Thr Glu Ala Phe Asn Lys Gly Arg Asn Glu Met Ile Gln Ser Glu			
420	425		430

aga tta tta gat tca aga ctt tca tct cct tca aat aat aat gga gat	1344
Arg Leu Leu Asp Ser Arg Leu Ser Ser Pro Ser Asn Asn Asn Gly Asp	
435 440 445	
tct aaa gaa gag aaa cga caa tta cgg gaa tca tta aga aac tca ggc	1392
Ser Lys Glu Glu Lys Arg Gln Leu Arg Glu Ser Leu Arg Asn Ser Gly	
450 455 460	
aat tat aaa gaa gga gtt act gat gat gcc ggt gga gct gca act ggt	1440
Asn Tyr Lys Glu Gly Val Thr Asp Asp Ala Gly Gly Ala Ala Thr Gly	
465 470 475 480	
ggg ggt agg aaa agt gcc ggt act cct aat aga aat agt act gat tac	1488
Gly Gly Arg Lys Ser Ala Gly Thr Pro Asn Arg Asn Ser Thr Asp Tyr	
485 490 495	
gtt tta cat gat ata tct gct cga gta cat tca cgt aat cga tca caa	1536
Val Leu His Asp Ile Ser Ala Arg Val His Ser Arg Asn Arg Ser Gln	
500 505 510	
gat tta ggg aat aat ttc aaa tta gct aat aat ggg aaa tca caa ttt	1584
Asp Leu Gly Asn Asn Phe Lys Leu Ala Asn Asn Gly Lys Ser Gln Phe	
515 520 525	
ttc aat gaa atc aaa act tta gaa gat cga tta gat gat gtt gac gtt	1632
Phe Asn Glu Ile Lys Thr Leu Glu Asp Arg Leu Asp Asp Val Asp Val	
530 535 540	
gaa ata tcg cat aat caa tat gct gaa gcc gtg gaa tta ata tca ata	1680
Glu Ile Ser His Asn Gln Tyr Ala Glu Ala Val Glu Leu Ile Ser Ile	
545 550 555 560	
att gaa tct aaa tta cgt aat att gaa aat gca tta act aat caa cgt	1728
Ile Glu Ser Lys Leu Arg Asn Ile Glu Asn Ala Leu Thr Asn Gln Arg	
565 570 575	
aat gga ggt aaa aat gtc aat att gct gat gaa tta tta ctt tta gat	1776
Asn Gly Gly Lys Asn Val Asn Ile Ala Asp Glu Leu Leu Leu Leu Asp	
580 585 590	
gta tca aaa ttg aaa att aaa aat cgg aaa gaa aat gta tct aat gga	1824
Val Ser Lys Leu Lys Ile Lys Asn Arg Lys Glu Asn Val Ser Asn Gly	
595 600 605	
tta ata ttt gat tta caa cat aat ata gct aaa ctt aaa caa gat gat	1872
Leu Ile Phe Asp Leu Gln His Asn Ile Ala Lys Leu Lys Gln Asp Asp	
610 615 620	
att gat aat att ttg acg tta ttt gat aat tta gag caa tta gat cga	1920
Ile Asp Asn Ile Leu Thr Leu Phe Asp Asn Leu Glu Gln Leu Asp Arg	
625 630 635 640	
ggg gtt caa gga tat ttg gat tca atg tca gct tat tta tca act aca	1968
Gly Val Gln Gly Tyr Leu Asp Ser Met Ser Ala Tyr Leu Ser Thr Thr	
645 650 655	

gta tca aaa tta att gtt ggt tta caa gga tca acg aaa atc gat gtt 2016
 Val Ser Lys Leu Ile Val Gly Leu Gln Gly Ser Thr Lys Ile Asp Val
 660 665 670

gtt aat tat ctt tcc aat tta atg gtt att aat gta tcg att gtg aaa 2064
 Val Asn Tyr Leu Ser Asn Leu Met Val Ile Asn Val Ser Ile Val Lys
 675 680 685

cgt aca att caa act tat gaa caa ata att gct cca att tta aaa cgt 2112
 Arg Thr Ile Gln Thr Tyr Glu Gln Ile Ile Ala Pro Ile Leu Lys Arg
 690 695 700

cat ggt gat gtt gat tca agt gga ttg att aat tgg tgt att gat gaa 2160
 His Gly Asp Val Asp Ser Ser Gly Leu Ile Asn Trp Cys Ile Asp Glu
 705 710 715 720

ttt act aaa ctt tgt aaa caa att aaa aaa cat ttg tat gga aca ttg 2208
 Phe Thr Lys Leu Cys Lys Gln Ile Lys Lys His Leu Tyr Gly Thr Leu
 725 730 735

ttg ata tct tct ggg att aat atg gaa act gat gaa cca att tat aaa 2256
 Leu Ile Ser Ser Gly Ile Asn Met Glu Thr Asp Glu Pro Ile Tyr Lys
 740 745 750

gtt aaa gaa aga aaa tta tat gat aat ttc ttg aag att atg caa cca 2304
 Val Lys Glu Arg Lys Leu Tyr Asp Asn Phe Leu Lys Ile Met Gln Pro
 755 760 765

caa ttg gaa gaa tta aaa ctg gtg gga tta aat gtt gat tat ata ttt 2352
 Gln Leu Glu Glu Leu Lys Leu Val Gly Leu Asn Val Asp Tyr Ile Phe
 770 775 780

gag tct ata tta aat ctt gaa 2373
 Glu Ser Ile Leu Asn Leu Glu
 785 790

<210> 6

<211> 791

<212> PRT

<213> Candida albicans

<400> 6

Met Asp Asn Leu Asp Pro Asn Ser Ser Leu Gln Val Glu Lys Leu Arg
1 5 10 15

Asn Arg Lys Ser Arg Ala Val Trp Gln Asn Asn Asn Thr Ser Thr His
20 25 30

Asn Asn Pro Tyr Ala Asn Leu Ser Thr Gly Glu Lys Ser Arg Ser Arg
35 40 45

His Asn Thr Gly Ser Ser Tyr Val Ser Pro Tyr Gly Gly Gly Asn Gly
50 55 60

Glu Glu Asn Ala Tyr Thr Gly Asn Asn Asn Lys Ser Asn Thr Ser Gly
65 70 75 80

Asn Leu Leu Gln Val Pro Gly Ala Gly Gly Gly Gly Asp Leu Asn Ser
 85 90 95

Asn Lys Lys Gln Ser Arg Arg Met Ser Ile His Val Ser Ala Arg Gln
 100 105 110

His Gly Arg Ser Phe Ser Gln Thr Gly Pro Ile Asp Met Ala Asn Leu
 115 120 125

Pro Ala Leu Pro Lys Ile Gly Gly Val Thr Thr Ser Gly Val Gly Gly
 130 135 140

Ala Gly Gly Asp Val Met Thr Arg Thr Gly Gly Leu Thr Ile Glu Gln
 145 150 155 160

Lys Ile Phe Lys Glu Leu Ser Gln Gly Ser Ala Ala Glu Val Asp Asp
 165 170 175

Tyr Tyr Lys Thr Leu Leu Lys Gln Lys Asn Leu Ile Thr Arg Asp Ile
 180 185 190

Lys Asp Asn Ile Asn Gln Asn Gln Lys Asn Ile Leu Gln Leu Thr Lys
 195 200 205

Asp Leu Lys Glu Thr Gln Glu Glu Leu Ile Glu Leu Arg Gly Thr Thr
 210 215 220

Lys Glu Leu Tyr Glu Val Leu Gly Tyr Phe Lys Glu Ser Ala Gln Arg
 225 230 235 240

Arg Leu Glu Leu Glu Phe Glu Pro Glu Thr Gln Lys Glu Leu His Leu
 245 250 255

Pro Gln Lys Ser Asn Gln Leu Gly Ile Pro Ser Asn Lys Lys Lys Asp
 260 265 270

Arg Ser Ser Ile Met Val Leu Lys Lys Met Trp Asp Ser Gln Leu Gln
 275 280 285

Ser Leu Phe Lys His Val Asp Gly Ala Ser Lys Phe Val Gln Pro Leu
 290 295 300

Pro Asn Arg His Ile Val Ala Glu Ser Gly Arg Trp Phe Glu Val Asn
 305 310 315 320

Val Gly Asn Trp Lys Pro Ser Tyr Pro Thr His Leu Phe Ile Phe Asn
 325 330 335

Asp Leu Ile Leu Ile Thr Val Lys Lys Ser Ser Ser Ser Ser Gln Glu
 340 345 350

Pro Thr Thr Gly Gly Ser Asn Gly Gly Ser Lys Ser Arg Leu Gln Ala
 355 360 365

Val Gln Cys Trp Pro Leu Thr Gln Val Ser Leu Gln Gln Ile Lys Ser
 370 375 380

Pro Lys Lys Asp Asp Asp Lys Met Tyr Phe Ile Asn Leu Lys Ser Lys
 385 390 395 400
 Ser Leu Ser Tyr Val Tyr Leu Thr Asp Arg Tyr Asp His Phe Val Lys
 405 410 415
 Val Thr Glu Ala Phe Asn Lys Gly Arg Asn Glu Met Ile Gln Ser Glu
 420 425 430
 Arg Leu Leu Asp Ser Arg Leu Ser Ser Pro Ser Asn Asn Asn Gly Asp
 435 440 445
 Ser Lys Glu Glu Lys Arg Gln Leu Arg Glu Ser Leu Arg Asn Ser Gly
 450 455 460
 Asn Tyr Lys Glu Gly Val Thr Asp Asp Ala Gly Gly Ala Ala Thr Gly
 465 470 475 480
 Gly Gly Arg Lys Ser Ala Gly Thr Pro Asn Arg Asn Ser Thr Asp Tyr
 485 490 495
 Val Leu His Asp Ile Ser Ala Arg Val His Ser Arg Asn Arg Ser Gln
 500 505 510
 Asp Leu Gly Asn Asn Phe Lys Leu Ala Asn Asn Gly Lys Ser Gln Phe
 515 520 525
 Phe Asn Glu Ile Lys Thr Leu Glu Asp Arg Leu Asp Asp Val Asp Val
 530 535 540
 Glu Ile Ser His Asn Gln Tyr Ala Glu Ala Val Glu Leu Ile Ser Ile
 545 550 555 560
 Ile Glu Ser Lys Leu Arg Asn Ile Glu Asn Ala Leu Thr Asn Gln Arg
 565 570 575
 Asn Gly Gly Lys Asn Val Asn Ile Ala Asp Glu Leu Leu Leu Leu Asp
 580 585 590
 Val Ser Lys Leu Lys Ile Lys Asn Arg Lys Glu Asn Val Ser Asn Gly
 595 600 605
 Leu Ile Phe Asp Leu Gln His Asn Ile Ala Lys Leu Lys Gln Asp Asp
 610 615 620
 Ile Asp Asn Ile Leu Thr Leu Phe Asp Asn Leu Glu Gln Leu Asp Arg
 625 630 635 640
 Gly Val Gln Gly Tyr Leu Asp Ser Met Ser Ala Tyr Leu Ser Thr Thr
 645 650 655
 Val Ser Lys Leu Ile Val Gly Leu Gln Gly Ser Thr Lys Ile Asp Val
 660 665 670
 Val Asn Tyr Leu Ser Asn Leu Met Val Ile Asn Val Ser Ile Val Lys
 675 680 685

Arg Thr Ile Gln Thr Tyr Glu Gln Ile Ile Ala Pro Ile Leu Lys Arg
690 695 700

His Gly Asp Val Asp Ser Ser Gly Leu Ile Asn Trp Cys Ile Asp Glu
705 710 715 720

Phe Thr Lys Leu Cys Lys Gln Ile Lys Lys His Leu Tyr Gly Thr Leu
725 730 735

Leu Ile Ser Ser Gly Ile Asn Met Glu Thr Asp Glu Pro Ile Tyr Lys
740 745 750

Val Lys Glu Arg Lys Leu Tyr Asp Asn Phe Leu Lys Ile Met Gln Pro
755 760 765

Gln Leu Glu Glu Leu Lys Leu Val Gly Leu Asn Val Asp Tyr Ile Phe
770 775 780

Glu Ser Ile Leu Asn Leu Glu
785 790

<210> 7

<211> 343

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Probe

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ttggtggttg ggtgtgtgtg gtccataagt atgccgtgtt gtcaccaccc ccagtcaata 120
ccattggcaa tttaggatgt gaaaaaatag taaatatact atcggtatgt ttatcaaaat 180
aagtccatga attgttggac atgtcaattt cttaaagtctc atgctcatca tctaattcca 240
tctctcatc ttcttcatcg ggtggcgctt gatcatcatc tgcaacttcc tcagccactt 300
cattaacatt gatataattct tcttgagtat cgtctacgac gtc 343

<210> 8

<211> 1248

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(1245)

<220>

<221> gene

<222> (1)..(1245)

<223> gene CaIR012

<400> 8

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Met Ser His Gln Gln Glu Asp Val Val Asp Asp Thr Gln Glu Glu Tyr	
1 5 10 15	
atc aat gtt aat gaa gtg gct gag gaa gtt gca gat gat gat caa gcg	96
Ile Asn Val Asn Glu Val Ala Glu Glu Val Ala Asp Asp Asp Gln Ala	
20 25 30	
cca ccc gat gaa gaa gat gag gag atg gaa tta gat gat gag cat gag	144
Pro Pro Asp Glu Glu Asp Glu Glu Met Glu Leu Asp Asp Glu His Glu	
35 40 45	
act tta gaa att gac atg tcc aac aat tca tgg act tat ttt gat aaa	192
Thr Leu Glu Ile Asp Met Ser Asn Asn Ser Trp Thr Tyr Phe Asp Lys	
50 55 60	
cat acc gat agt ata ttt act att ttt tca cat cct aaa ttg cca atg	240
His Thr Asp Ser Ile Phe Thr Ile Phe Ser His Pro Lys Leu Pro Met	
65 70 75 80	
gta ttg act ggg ggt ggt gac aac acg gca tac tta tgg acc aca cac	288
Val Leu Thr Gly Gly Gly Asp Asn Thr Ala Tyr Leu Trp Thr Thr His	
85 90 95	
acc caa cca cca aga ttt gtt ggc gaa atc act gga cat aaa gag tct	336
Thr Gln Pro Pro Arg Phe Val Gly Glu Ile Thr Gly His Lys Glu Ser	
100 105 110	
gtt ata tct gga ggg ttt act gca gac ggc aag ttt gtt gtt act gca	384
Val Ile Ser Gly Gly Phe Thr Ala Asp Gly Lys Phe Val Val Thr Ala	
115 120 125	
gac atg aat gga tta att caa gtt ttc aaa gcc aca aaa gga ggt gaa	432
Asp Met Asn Gly Leu Ile Gln Val Phe Lys Ala Thr Lys Gly Gly Glu	
130 135 140	
cag tgg gtg aaa ttt ggt gaa ttg gac gaa gtt gaa gaa gtg ttg ttt	480
Gln Trp Val Lys Phe Gly Glu Leu Asp Glu Val Glu Glu Val Leu Phe	
145 150 155 160	
gtt act gtg cat cca aca tta cca ttc ttt gcc ttt ggt gct acc gat	528
Val Thr Val His Pro Thr Leu Pro Phe Phe Ala Phe Gly Ala Thr Asp	
165 170 175	
gga tct ata tgg gtc tac caa ata gac gaa tcc agt aaa ctg cta gtg	576
Gly Ser Ile Trp Val Tyr Gln Ile Asp Glu Ser Ser Lys Leu Leu Val	
180 185 190	
caa att atg tct ggg ttc tca cac aca tta gaa tgt aat ggt gct gta	624
Gln Ile Met Ser Gly Phe Ser His Thr Leu Glu Cys Asn Gly Ala Val	
195 200 205	
ttt ata caa gga aaa gat gaa aat gat ttg aca ttg gtc tct ata agt	672
Phe Ile Gln Gly Lys Asp Glu Asn Asp Leu Thr Leu Val Ser Ile Ser	

210	215	220	
gaa gat ggt act gtg gtg aac tgg aac tgt ttt aca gga caa gtg aat			720
Glu Asp Gly Thr Val Val Asn Trp Asn Cys Phe Thr Gly Gln Val Asn			
225	230	235	240
tat aaa ttg caa cct cat gat gac ttt aaa gga gtt gaa agt ccg tgg			768
Tyr Lys Leu Gln Pro His Asp Asp Phe Lys Gly Val Glu Ser Pro Trp			
	245	250	255
gtc acg gtc aaa gta cat ggt aat ctt gtg gcc att ggt ggc aga gat			816
Val Thr Val Lys Val His Gly Asn Leu Val Ala Ile Gly Gly Arg Asp			
	260	265	270
ggc cag cta tca att gtg aac aat gac act ggt aaa atc gtt cat act			864
Gly Gln Leu Ser Ile Val Asn Asn Asp Thr Gly Lys Ile Val His Thr			
	275	280	285
ctt aaa aca ttg gat aat gtc gac gac att gca gaa ctc tca att gag			912
Leu Lys Thr Leu Asp Asn Val Asp Asp Ile Ala Glu Leu Ser Ile Glu			
	290	295	300
gca ttg agt tgg tgt gaa agc aaa aat att aac ctc ttg gca gtg ggt			960
Ala Leu Ser Trp Cys Glu Ser Lys Asn Ile Asn Leu Leu Ala Val Gly			
305	310	315	320
ttg gtt tct ggt gac gtt tta tta ttt gat act cag caa tgg aga ttg			1008
Leu Val Ser Gly Asp Val Leu Leu Phe Asp Thr Gln Gln Trp Arg Leu			
	325	330	335
aga aag aac ttg aaa gtt gac gat gcc atc acc aaa tta caa ttt gtt			1056
Arg Lys Asn Leu Lys Val Asp Asp Ala Ile Thr Lys Leu Gln Phe Val			
	340	345	350
ggc gaa acc ccc att ttg gtg gga agt agt atg gat ggt aaa att tac			1104
Gly Glu Thr Pro Ile Leu Val Gly Ser Ser Met Asp Gly Lys Ile Tyr			
	355	360	365
aaa tgg gac gct aga act ggt gaa gag ttg ttt gct ggt gtg gga cac			1152
Lys Trp Asp Ala Arg Thr Gly Glu Glu Leu Phe Ala Gly Val Gly His			
	370	375	380
aac atg gga gta ttg gac ttt gct att tta gat gga ggt aaa aag ttg			1200
Asn Met Gly Val Leu Asp Phe Ala Ile Leu Asp Gly Gly Lys Lys Leu			
385	390	395	400
gtt act gct ggt gat gaa ggt gtt tca ttg gtc ttt gta cat gaa tag			1248
Val Thr Ala Gly Asp Glu Gly Val Ser Leu Val Phe Val His Glu			
	405	410	415

<210> 9

<211> 415

<212> PRT

<213> Candida albicans

<400> 9

Met Ser His Gln Gln Glu Asp Val Val Asp Asp Thr Gln Glu Glu Tyr
 1 5 10 15
 Ile Asn Val Asn Glu Val Ala Glu Glu Val Ala Asp Asp Asp Gln Ala
 20 25 30
 Pro Pro Asp Glu Glu Asp Glu Glu Met Glu Leu Asp Asp Glu His Glu
 35 40 45
 Thr Leu Glu Ile Asp Met Ser Asn Asn Ser Trp Thr Tyr Phe Asp Lys
 50 55 60
 His Thr Asp Ser Ile Phe Thr Ile Phe Ser His Pro Lys Leu Pro Met
 65 70 75 80
 Val Leu Thr Gly Gly Gly Asp Asn Thr Ala Tyr Leu Trp Thr Thr His
 85 90 95
 Thr Gln Pro Pro Arg Phe Val Gly Glu Ile Thr Gly His Lys Glu Ser
 100 105 110
 Val Ile Ser Gly Gly Phe Thr Ala Asp Gly Lys Phe Val Val Thr Ala
 115 120 125
 Asp Met Asn Gly Leu Ile Gln Val Phe Lys Ala Thr Lys Gly Gly Glu
 130 135 140
 Gln Trp Val Lys Phe Gly Glu Leu Asp Glu Val Glu Glu Val Leu Phe
 145 150 155 160
 Val Thr Val His Pro Thr Leu Pro Phe Phe Ala Phe Gly Ala Thr Asp
 165 170 175
 Gly Ser Ile Trp Val Tyr Gln Ile Asp Glu Ser Ser Lys Leu Leu Val
 180 185 190
 Gln Ile Met Ser Gly Phe Ser His Thr Leu Glu Cys Asn Gly Ala Val
 195 200 205
 Phe Ile Gln Gly Lys Asp Glu Asn Asp Leu Thr Leu Val Ser Ile Ser
 210 215 220
 Glu Asp Gly Thr Val Val Asn Trp Asn Cys Phe Thr Gly Gln Val Asn
 225 230 235 240
 Tyr Lys Leu Gln Pro His Asp Asp Phe Lys Gly Val Glu Ser Pro Trp
 245 250 255
 Val Thr Val Lys Val His Gly Asn Leu Val Ala Ile Gly Gly Arg Asp
 260 265 270
 Gly Gln Leu Ser Ile Val Asn Asn Asp Thr Gly Lys Ile Val His Thr
 275 280 285
 Leu Lys Thr Leu Asp Asn Val Asp Asp Ile Ala Glu Leu Ser Ile Glu
 290 295 300

Ala Leu Ser Trp Cys Glu Ser Lys Asn Ile Asn Leu Leu Ala Val Gly
305 310 315 320

Leu Val Ser Gly Asp Val Leu Leu Phe Asp Thr Gln Gln Trp Arg Leu
325 330 335

Arg Lys Asn Leu Lys Val Asp Asp Ala Ile Thr Lys Leu Gln Phe Val
340 345 350

Gly Glu Thr Pro Ile Leu Val Gly Ser Ser Met Asp Gly Lys Ile Tyr
355 360 365

Lys Trp Asp Ala Arg Thr Gly Glu Glu Leu Phe Ala Gly Val Gly His
370 375 380

Asn Met Gly Val Leu Asp Phe Ala Ile Leu Asp Gly Gly Lys Lys Leu
385 390 395 400

Val Thr Ala Gly Asp Glu Gly Val Ser Leu Val Phe Val His Glu
405 410 415

<210> 10

<211> 5544

<212> DNA

<213> Candida albicans

<220>

<221> CDS

<222> (1)..(5541)

<220>

<221> gene

<222> (1)..(5541)

<223> gene CaJL039

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Met Ser Gly Ile Phe Asn Trp Ser Leu Asp Val Phe Ala Asp Ile Tyr
1 5 10 15

aac acc ctc aag ttt gag tcc aat ata gat ttg gat aca atc gac ttc 96
Asn Thr Leu Lys Phe Glu Ser Asn Ile Asp Leu Asp Thr Ile Asp Phe
20 25 30

acc agc atc aag aat gat ctt gca aat gtt ttg att aca cca gtc cct 144
Thr Ser Ile Lys Asn Asp Leu Ala Asn Val Leu Ile Thr Pro Val Pro
35 40 45

ctg gat caa tca cgt agc aaa ctt gga gac gca tca aaa cca gtg gcg 192
Leu Asp Gln Ser Arg Ser Lys Leu Gly Asp Ala Ser Lys Pro Val Ala
50 55 60

ttg ccc agt gga gat gag gtg aaa ttg aat caa gca tca att gaa att 240
Leu Pro Ser Gly Asp Glu Val Lys Leu Asn Gln Ala Ser Ile Glu Ile
65 70 75 80

act gga gtt tta tca aat gaa ttg gat tta gat gaa cta aat aca gca	288
Thr Gly Val Leu Ser Asn Glu Leu Asp Leu Asp Glu Leu Asn Thr Ala	
85 90 95	
gag ttg tta tat aac gca agt gac ttg agc tac aag aag gga acg tcc	336
Glu Leu Leu Tyr Asn Ala Ser Asp Leu Ser Tyr Lys Lys Gly Thr Ser	
100 105 110	
att ggc gat agt gct cga ttg gct tat tat tta aga gct cat tat ata	384
Ile Gly Asp Ser Ala Arg Leu Ala Tyr Tyr Leu Arg Ala His Tyr Ile	
115 120 125	
cta aac att gtt gga tac tta gtt tcg cat aaa cgt tta gat atc atc	432
Leu Asn Ile Val Gly Tyr Leu Val Ser His Lys Arg Leu Asp Ile Ile	
130 135 140	
act aac aac aac caa gtg ttg ttt gac aat att ttg aaa agt ttc agc	480
Thr Asn Asn Asn Gln Val Leu Phe Asp Asn Ile Leu Lys Ser Phe Ser	
145 150 155 160	
aag att tat act ttg agt ggt aaa tta aat gac atg att gac aag caa	528
Lys Ile Tyr Thr Leu Ser Gly Lys Leu Asn Asp Met Ile Asp Lys Gln	
165 170 175	
aaa gtt acc ggc gac atc aac aat ctt gca ttt atc aat tgt atc aat	576
Lys Val Thr Gly Asp Ile Asn Asn Leu Ala Phe Ile Asn Cys Ile Asn	
180 185 190	
tat tcc aga agt cag ttg ttt aat gca cac gag tta ttg gga caa gtt	624
Tyr Ser Arg Ser Gln Leu Phe Asn Ala His Glu Leu Leu Gly Gln Val	
195 200 205	
gta ttt gga tta gcg gat aat tat tat gag agt tat ggc aca cta aac	672
Val Phe Gly Leu Ala Asp Asn Tyr Tyr Glu Ser Tyr Gly Thr Leu Asn	
210 215 220	
aac tat aat tcc tta gtg gag ttt ata ctg aaa aat atc agc gat gaa	720
Asn Tyr Asn Ser Leu Val Glu Phe Ile Leu Lys Asn Ile Ser Asp Glu	
225 230 235 240	
gat gtt ttt gtt atc cat ttt tta cca tcc act tta caa ttg ttc aag	768
Asp Val Phe Val Ile His Phe Leu Pro Ser Thr Leu Gln Leu Phe Lys	
245 250 255	
aaa tta ctt caa cta ggt gag gaa tct tta gtc gat cag ttt tac aag	816
Lys Leu Leu Gln Leu Gly Glu Glu Ser Leu Val Asp Gln Phe Tyr Lys	
260 265 270	
act ata acc tct tcc ata cta aaa gat tat gaa gcc aac aat ttt tcc	864
Thr Ile Thr Ser Ser Ile Leu Lys Asp Tyr Glu Ala Asn Asn Phe Ser	
275 280 285	
aaa agt gaa gat att gac ttg tca aaa tca aaa ttg tct ggc ttt gaa	912
Lys Ser Glu Asp Ile Asp Leu Ser Lys Ser Lys Leu Ser Gly Phe Glu	
290 295 300	
ata gtc aca agc ttt att ttt cta act gag ttt att cca tgg tgc aag	960

Ile Val Thr Ser Phe	Ile Phe Leu Thr Glu Phe Ile Pro Trp Cys Lys	305	310	315	320
cag ctg tca agt aga acc gcg aaa tac gat ttc aaa gat gat ata tta	Gln Leu Ser Ser Arg Thr Ala Lys Tyr Asp Phe Lys Asp Asp Ile Leu	1008	325	330	335
aag tat atg gaa ttc ttg ata agt tat gga gtt atg gaa cga tta tta	Lys Tyr Met Glu Phe Leu Ile Ser Tyr Gly Val Met Glu Arg Leu Leu	1056	340	345	350
tca tac tgt tct gaa acc agc aat gca aaa act cag caa gtg tac gac	Ser Tyr Cys Ser Glu Thr Ser Asn Ala Lys Thr Gln Gln Val Tyr Asp	1104	355	360	365
tgg tca aac atg tac gat ttc aga gca ttg ctt caa aag aat ttc cca	Trp Ser Asn Met Tyr Asp Phe Arg Ala Leu Leu Gln Lys Asn Phe Pro	1152	370	375	380
cga ctt aca cca gca aaa ttt cat tat cct ggc aat caa gaa ttg ttg	Arg Leu Thr Pro Ala Lys Phe His Tyr Pro Gly Asn Gln Glu Leu Leu	1200	385	390	400
aat gca gtt aga ccg gga tat gaa aat ata tcc aaa ttg att gac att	Asn Ala Val Arg Pro Gly Tyr Glu Asn Ile Ser Lys Leu Ile Asp Ile	1248	405	410	415
tcc ttt ttg acg tta gat cca tcg ctt aat gag acg ttg gtt tca cct	Ser Phe Leu Thr Leu Asp Pro Ser Leu Asn Glu Thr Leu Val Ser Pro	1296	420	425	430
ttt ttc cag agc ttt ttc agt gtg ttt ata tct aat gcc gca gtt gtt	Phe Phe Gln Ser Phe Phe Ser Val Phe Ile Ser Asn Ala Ala Val Val	1344	435	440	445
atg acc tct tta agg gac tca gag gaa gat ttt gtt tta tcg tcg ttg	Met Thr Ser Leu Arg Asp Ser Glu Glu Asp Phe Val Leu Ser Ser Leu	1392	450	455	460
aat gaa agt gac gaa gag gaa gaa gaa gaa gaa agc gac agc gac gaa	Asn Glu Ser Asp Glu Glu Glu Glu Glu Glu Glu Ser Asp Ser Asp Glu	1440	465	470	475
gat tct tcg acc cca aaa aac aaa gaa aaa tca gct ggg tta gac ctt	Asp Ser Ser Thr Pro Lys Asn Lys Glu Lys Ser Ala Gly Leu Asp Leu	1488	485	490	495
gac aag att gcc cag cgt gct gaa tta gaa agg ttc tac ttg gct ttc	Asp Lys Ile Ala Gln Arg Ala Glu Leu Glu Arg Phe Tyr Leu Ala Phe	1536	500	505	510
gcg tac acc tac aac aat cga cct gaa ttg tgt gcg tta ttt tgg ggg	Ala Tyr Thr Tyr Asn Asn Arg Pro Glu Leu Cys Ala Leu Phe Trp Gly	1584	515	520	525
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Ala	Asn	Asn	Thr	Ser	Pro	Leu	Ile	Thr	Ala	Thr	Phe	Cys	Leu	Leu	Leu	
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Gly	Ser	Leu	Ala	Ser	Ala	Gly	Ala	Glu	Ala	Thr	Ser	Arg	Ile	Trp	Glu	
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Ser	Lys	Val	Ser	Val	Asp	Ser	Leu	Tyr	Asp	Ser	Leu	Lys	Tyr	Tyr	Ile	
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Asp	Ser	Leu	Asn	Glu	Ser	Phe	Glu	Gln	Asp	Leu	Asn	Ala	Gln	Leu	Met	
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Leu	Asn	Gln	Lys	Lys	Gln	Asp	Phe	Leu	Phe	Ser	Thr	Thr	Thr	Ser	Lys	
625					630					635					640	
cag	gac	ctt	gat	gat	tct	ggc	gag	aat	aga	att	gtt	ata	gag	ttg	gcc	1968
Gln	Asp	Leu	Asp	Asp	Ser	Gly	Glu	Asn	Arg	Ile	Val	Ile	Glu	Leu	Ala	
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gag	gat	tca	ctt	gtc	ctc	att	tca	ggg	ttt	att	caa	tta	ctt	tct	gca	2016
Glu	Asp	Ser	Leu	Val	Leu	Ile	Ser	Gly	Phe	Ile	Gln	Leu	Leu	Ser	Ala	
			660					665					670			
att	gtg	aag	aat	ttg	aac	act	aag	aat	gaa	aga	agc	aaa	gaa	atc	aaa	2064
Ile	Val	Lys	Asn	Leu	Asn	Thr	Lys	Asn	Glu	Arg	Ser	Lys	Glu	Ile	Lys	
		675					680					685				
tcc	gtg	gta	tac	act	aga	ttc	tca	cca	atc	att	aaa	ggg	ttt	tta	aaa	2112
Ser	Val	Val	Tyr	Thr	Arg	Phe	Ser	Pro	Ile	Ile	Lys	Gly	Phe	Leu	Lys	
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ttc	gat	aat	ttg	atc	aat	ggg	agc	agg	ttc	ctt	caa	gtt	gat	gct	agc	2160
Phe	Asp	Asn	Leu	Ile	Asn	Gly	Ser	Arg	Phe	Leu	Gln	Val	Asp	Ala	Ser	
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att	caa	agc	aca	aac	aac	ccc	aaa	ttt	att	gat	ttg	cca	aat	gtt	ttc	2208
Ile	Gln	Ser	Thr	Asn	Asn	Pro	Lys	Phe	Ile	Asp	Leu	Pro	Asn	Val	Phe	
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gtc	agt	gat	gac	tcg	aga	att	ata	ttg	acg	aac	ctc	att	cta	acc	ttt	2256
Val	Ser	Asp	Asp	Ser	Arg	Ile	Ile	Leu	Thr	Asn	Leu	Ile	Leu	Thr	Phe	
			740					745					750			
tta	ggc	gat	ttt	gtt	acc	aac	gat	agt	gat	ccg	tat	att	aga	tat	gag	2304
Leu	Gly	Asp	Phe	Val	Thr	Asn	Asp	Ser	Asp	Pro	Tyr	Ile	Arg	Tyr	Glu	
		755					760						765			

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Ile Trp Arg Leu Val Asp Arg Trp Met Tyr Gln Gly Leu His Ser Leu	
770 775 780	
cca gaa gac aag aaa gat gat gct ttt aga cat att aag aga aag tat	2400
Pro Glu Asp Lys Lys Asp Asp Ala Phe Arg His Ile Lys Arg Lys Tyr	
785 790 795 800	
aac agt aag aaa aat gtt ccc atc aat caa gca ttt tca aca aac cta	2448
Asn Ser Lys Lys Asn Val Pro Ile Asn Gln Ala Phe Ser Thr Asn Leu	
805 810 815	
act cat ctt agt caa att ggg aat ttc act gtc ttg gtg aaa aaa ttg	2496
Thr His Leu Ser Gln Ile Gly Asn Phe Thr Val Leu Val Lys Lys Leu	
820 825 830	
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Leu Thr Pro Tyr Ala Asp Ser Asn Glu Ala Phe Thr Lys Tyr Ser Leu	
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Leu Tyr Pro Cys Asp Leu Gly Leu Gly Tyr Arg Phe Asn Asn Gln Leu	
850 855 860	
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Gly Ile Trp Pro Tyr Ile Glu Phe Leu Met Gln Asn Val Phe Ala Asn	
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Ser Gly Thr Ile Ala Asn Lys Arg Asp Arg Val Asn Leu Gln Leu Asn	
885 890 895	
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Leu Leu Glu Leu Phe Ser Asn Ala Leu Gln Gly Val Asp Trp Lys Phe	
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ctt att gat gtg gca ccg aaa att att cgt gac ttg aaa aat ttt aat	2784
Leu Ile Asp Val Ala Pro Lys Ile Ile Arg Asp Leu Lys Asn Phe Asn	
915 920 925	
ggg ata ttt gac tcg ctt att cct ggt gtt caa ttg gac ttt gaa gtg	2832
Gly Ile Phe Asp Ser Leu Ile Pro Gly Val Gln Leu Asp Phe Glu Val	
930 935 940	
ttt gtc aaa ttg cat cat tca gtt gct gtg att aac tat cta ttt gaa	2880
Phe Val Lys Leu His His Ser Val Ala Val Ile Asn Tyr Leu Phe Glu	
945 950 955 960	
aac agg aca ttt tct gcc ttg ttt aag ctt gtt aat att gga gtt gat	2928
Asn Arg Thr Phe Ser Ala Leu Phe Lys Leu Val Asn Ile Gly Val Asp	
965 970 975	
tct gtg aat gaa tca ggt gaa tcg gcg gaa ttg gtg tca cat gcc ctt	2976
Ser Val Asn Glu Ser Gly Glu Ser Ala Glu Leu Val Ser His Ala Leu	
980 985 990	

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Gly Leu Ile Asn Ser Leu Leu Arg Val Gln Asn Ser Phe Ile Asn Lys	
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Leu Leu Pro Ile Leu Arg Asn Lys Asp Thr Gln Gln Gln Leu His Arg	
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Gly Thr Ala Ile Gly Ile Gly Thr Ser Met Ser Leu Ala Leu Ala Thr	
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Pro Arg Thr Ile Phe Asp Cys Ile Tyr Tyr Pro Lys Asn Leu Gly Thr	
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His Gly Val Ala Asp Phe Tyr Glu Val Ile Leu Phe His Leu Ser Ala	
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Val Val Gln Phe Ala Leu Tyr Val Ser Cys Glu Asn Thr Ile Ser Asn	
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Lys Ala Ile Ser Ile Leu Lys Gly Val Ser Gln Ser Lys Phe Phe Val	
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acc aga gtt tca agc tct gct gat ccc tta ctc aac aac gat aga ttg	3360
Thr Arg Val Ser Ser Ser Ala Asp Pro Leu Leu Asn Asn Asp Arg Leu	
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att acc aca ttt gaa aac atc gac gag tca ata aaa atc aag ttt gct	3408
Ile Thr Thr Phe Glu Asn Ile Asp Glu Ser Ile Lys Ile Lys Phe Ala	
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ttc att gac aag ttt gaa gaa ctc gag gac tct ttg aat atg aaa tat	3456
Phe Ile Asp Lys Phe Glu Glu Leu Glu Asp Ser Leu Asn Met Lys Tyr	
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gag ata ttg gat ttt gtt ttg ggc aat ctc aat caa ttt gat ggc aaa	3504
Glu Ile Leu Asp Phe Val Leu Gly Asn Leu Asn Gln Phe Asp Gly Lys	
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Val Ala Thr Thr Ala His Phe Leu Leu Gly Tyr Lys Val Lys Gly Asp	
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Thr Leu Asp Leu Val Gln Thr Asn Asp Gln Asn Thr Leu Leu Lys Ser	
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Phe Leu Asn Thr Leu Ser Ile Ser Leu Asp Leu Ile Ser Glu Ile Asp	
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Tyr Asn Asn Gly Asn Asn His Ile Ile Asp Val Gly Pro Ala Lys Leu	
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Ser Ser Leu Ile Leu Gln Ile Leu Ile Lys Leu Cys Gln Asp Pro Ile	
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Ser Ser Ser Ile Thr Leu Asn Gln Leu Arg Glu Tyr Glu Glu Leu Phe	
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gaa aaa ttg gtt aac tgt caa cct aaa ctt gat ttg aat acc gtt tgg	3840
Glu Lys Leu Val Asn Cys Gln Pro Lys Leu Asp Leu Asn Thr Val Trp	
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Cys Gly Asn Gln Phe Asp Gly Asp Leu Gln Ile Asp Ala Ser Asn Val	
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Phe Val Asp Asn Gln Ala Ser Thr Gln Ala Phe Phe Ser Phe Ile Asn	
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Gln Arg Asn Leu Ile Leu Gln Tyr Leu Ser Leu Glu Phe His Ser Val	
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Lys Ser Arg Thr Lys Arg Glu Tyr Tyr Ser Lys Val Leu Thr Asn Asp	
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Lys Glu Phe Val Asn Arg Thr Pro Lys Val Leu Thr Phe Leu Asn Ile	
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Leu Asn Tyr Ser Phe Lys Asn Phe Glu Val Gln Lys Tyr Glu Trp Leu	
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gcc gaa gaa att atg gtt gaa gga agt aag att tct gac ttt gtc aca	4320
Ala Glu Glu Ile Met Val Glu Gly Ser Lys Ile Ser Asp Phe Val Thr	
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Lys Tyr Leu Val Ser Thr Asp Leu Lys Asp Val Gln Leu Lys Cys Leu	

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His Ser Trp Cys Gln Leu Ile Glu Ile Leu Val Thr Asp Ser Gly Ile			
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Asn Ser Leu Asn Phe Ile Leu Glu Val Leu Gln Val Ile Ile Pro Lys			
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Ile Asn Asp Tyr Phe Asp Val Asp Ile Leu Phe Ser Glu Glu Met Val			
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Ser Leu Cys Val Leu Leu Phe Asp Leu Tyr Asp Gln Leu Thr Leu Ala			
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Asp Arg Lys Gly Glu Asp Phe Ala Leu Gly Ile Glu Arg Leu Ile Pro			
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Leu Phe Gln Thr Cys Ile Ala Gly Ile Leu Asn Ser Asn Ser Thr Pro			
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Ser Leu Arg Ser Asp Leu Tyr Val Val Gly Asn Lys Phe Leu Leu Lys			
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Cys Phe Glu Arg Glu Ser Phe Leu Lys Gln Val Met His Ile Ile Lys			
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Ser Val Asp Lys Lys Phe Phe Gln Val Ile Cys Asn Asp Ala Ile Tyr			
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Ile Lys Asn Asn Ala Leu Leu Leu Leu Val Arg Ser Val Lys Arg Thr			
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Asp Ala Met Ile Lys Leu Cys Gln Glu Lys Asn Ser Gly Val Thr Leu			
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Asp His Phe Ile Phe Asp Leu Met Ala Phe Lys Ala Thr Leu Tyr Phe			
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Phe Val Arg Val Ala Lys Ser Lys Asn Gly Ala Leu Gln Leu Ile Gln
1685 1690 1695

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Pro Asp Ile Gly Leu Ser Leu Arg Ile Glu Glu Val Gln Asp His Lys
1715 1720 1725

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1745 1750 1755 1760

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1765 1770 1775

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1780 1785 1790

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Thr Ser Ile Lys Asn Asp Leu Ala Asn Val Leu Ile Thr Pro Val Pro
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 Leu Asp Gln Ser Arg Ser Lys Leu Gly Asp Ala Ser Lys Pro Val Ala
 50 55 60
 Leu Pro Ser Gly Asp Glu Val Lys Leu Asn Gln Ala Ser Ile Glu Ile
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 Thr Gly Val Leu Ser Asn Glu Leu Asp Leu Asp Glu Leu Asn Thr Ala
 85 90 95
 Glu Leu Leu Tyr Asn Ala Ser Asp Leu Ser Tyr Lys Lys Gly Thr Ser
 100 105 110
 Ile Gly Asp Ser Ala Arg Leu Ala Tyr Tyr Leu Arg Ala His Tyr Ile
 115 120 125
 Leu Asn Ile Val Gly Tyr Leu Val Ser His Lys Arg Leu Asp Ile Ile
 130 135 140
 Thr Asn Asn Asn Gln Val Leu Phe Asp Asn Ile Leu Lys Ser Phe Ser
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 Tyr Ser Arg Ser Gln Leu Phe Asn Ala His Glu Leu Leu Gly Gln Val
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 Val Phe Gly Leu Ala Asp Asn Tyr Tyr Glu Ser Tyr Gly Thr Leu Asn
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 Asn Tyr Asn Ser Leu Val Glu Phe Ile Leu Lys Asn Ile Ser Asp Glu
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 Asp Val Phe Val Ile His Phe Leu Pro Ser Thr Leu Gln Leu Phe Lys
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 Lys Leu Leu Gln Leu Gly Glu Glu Ser Leu Val Asp Gln Phe Tyr Lys
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 Lys Ser Glu Asp Ile Asp Leu Ser Lys Ser Lys Leu Ser Gly Phe Glu
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 Ile Val Thr Ser Phe Ile Phe Leu Thr Glu Phe Ile Pro Trp Cys Lys
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Lys Tyr Met Glu Phe Leu Ile Ser Tyr Gly Val Met Glu Arg Leu Leu
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 465 470 475 480
 Asp Ser Ser Thr Pro Lys Asn Lys Glu Lys Ser Ala Gly Leu Asp Leu
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 Ser Val Val Tyr Thr Arg Phe Ser Pro Ile Ile Lys Gly Phe Leu Lys
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 835 840 845
 Leu Tyr Pro Cys Asp Leu Gly Leu Gly Tyr Arg Phe Asn Asn Gln Leu
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 Gly Ile Trp Pro Tyr Ile Glu Phe Leu Met Gln Asn Val Phe Ala Asn
 865 870 875 880
 Ser Gly Thr Ile Ala Asn Lys Arg Asp Arg Val Asn Leu Gln Leu Asn
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 Leu Ile Asp Val Ala Pro Lys Ile Ile Arg Asp Leu Lys Asn Phe Asn
 915 920 925
 Gly Ile Phe Asp Ser Leu Ile Pro Gly Val Gln Leu Asp Phe Glu Val
 930 935 940

Phe Val Lys Leu His His Ser Val Ala Val Ile Asn Tyr Leu Phe Glu
 945 950 955 960
 Asn Arg Thr Phe Ser Ala Leu Phe Lys Leu Val Asn Ile Gly Val Asp
 965 970 975
 Ser Val Asn Glu Ser Gly Glu Ser Ala Glu Leu Val Ser His Ala Leu
 980 985 990
 Gly Leu Ile Asn Ser Leu Leu Arg Val Gln Asn Ser Phe Ile Asn Lys
 995 1000 1005
 Leu Leu Pro Ile Leu Arg Asn Lys Asp Thr Gln Gln Gln Leu His Arg
 1010 1015 1020
 Gly Thr Ala Ile Gly Ile Gly Thr Ser Met Ser Leu Ala Leu Ala Thr
 1025 1030 1035 1040
 Pro Arg Thr Ile Phe Asp Cys Ile Tyr Tyr Pro Lys Asn Leu Gly Thr
 1045 1050 1055
 His Gly Val Ala Asp Phe Tyr Glu Val Ile Leu Phe His Leu Ser Ala
 1060 1065 1070
 Val Val Gln Phe Ala Leu Tyr Val Ser Cys Glu Asn Thr Ile Ser Asn
 1075 1080 1085
 Lys Ala Ile Ser Ile Leu Lys Gly Val Ser Gln Ser Lys Phe Phe Val
 1090 1095 1100
 Thr Arg Val Ser Ser Ser Ala Asp Pro Leu Leu Asn Asn Asp Arg Leu
 1105 1110 1115 1120
 Ile Thr Thr Phe Glu Asn Ile Asp Glu Ser Ile Lys Ile Lys Phe Ala
 1125 1130 1135
 Phe Ile Asp Lys Phe Glu Glu Leu Glu Asp Ser Leu Asn Met Lys Tyr
 1140 1145 1150
 Glu Ile Leu Asp Phe Val Leu Gly Asn Leu Asn Gln Phe Asp Gly Lys
 1155 1160 1165
 Val Ala Thr Thr Ala His Phe Leu Leu Gly Tyr Lys Val Lys Gly Asp
 1170 1175 1180
 Thr Leu Asp Leu Val Gln Thr Asn Asp Gln Asn Thr Leu Leu Lys Ser
 1185 1190 1195 1200
 Phe Leu Asn Thr Leu Ser Ile Ser Leu Asp Leu Ile Ser Glu Ile Asp
 1205 1210 1215
 Tyr Asn Asn Gly Asn Asn His Ile Ile Asp Val Gly Pro Ala Lys Leu
 1220 1225 1230
 Ser Ser Leu Ile Leu Gln Ile Leu Ile Lys Leu Cys Gln Asp Pro Ile
 1235 1240 1245

Ser Ser Ser Ile Thr Leu Asn Gln Leu Arg Glu Tyr Glu Glu Leu Phe
 1250 1255 1260
 Glu Lys Leu Val Asn Cys Gln Pro Lys Leu Asp Leu Asn Thr Val Trp
 265 1270 1275 1280
 Cys Gly Asn Gln Phe Asp Gly Asp Leu Gln Ile Asp Ala Ser Asn Val
 1285 1290 1295
 Phe Val Asp Asn Gln Ala Ser Thr Gln Ala Phe Phe Ser Phe Ile Asn
 1300 1305 1310
 Gln Arg Asn Leu Ile Leu Gln Tyr Leu Ser Leu Glu Phe His Ser Val
 1315 1320 1325
 Lys Ser Arg Thr Lys Arg Glu Tyr Tyr Ser Lys Val Leu Thr Asn Asp
 1330 1335 1340
 Lys Glu Phe Val Asn Arg Thr Pro Lys Val Leu Thr Phe Leu Asn Ile
 345 1350 1355 1360
 Leu Asn Tyr Ser Phe Lys Asn Phe Glu Val Gln Lys Tyr Glu Trp Leu
 1365 1370 1375
 Asp Gln Lys Phe Asn Val Ser Leu Leu Leu Ala Glu Val Asn Ala Gln
 1380 1385 1390
 Lys Asn Gly Thr Leu Asp Phe Ser Val Leu Thr Lys Val Phe Arg Leu
 1395 1400 1405
 Leu Cys Gln Thr Ser Asn Leu Ile Thr Pro Glu Ser Lys Gln Leu Phe
 1410 1415 1420
 Ala Glu Glu Ile Met Val Glu Gly Ser Lys Ile Ser Asp Phe Val Thr
 425 1430 1435 1440
 Lys Tyr Leu Val Ser Thr Asp Leu Lys Asp Val Gln Leu Lys Cys Leu
 1445 1450 1455
 His Ser Trp Cys Gln Leu Ile Glu Ile Leu Val Thr Asp Ser Gly Ile
 1460 1465 1470
 Asn Ser Leu Asn Phe Ile Leu Glu Val Leu Gln Val Ile Ile Pro Lys
 1475 1480 1485
 Ile Asn Asp Tyr Phe Asp Val Asp Ile Leu Phe Ser Glu Glu Met Val
 1490 1495 1500
 Ser Leu Cys Val Leu Leu Phe Asp Leu Tyr Asp Gln Leu Thr Leu Ala
 505 1510 1515 1520
 Asp Arg Lys Gly Glu Asp Phe Ala Leu Gly Ile Glu Arg Leu Ile Pro
 1525 1530 1535
 Leu Phe Gln Thr Cys Ile Ala Gly Ile Leu Asn Ser Asn Ser Thr Pro
 1540 1545 1550

Ser Leu Arg Ser Asp Leu Tyr Val Val Gly Asn Lys Phe Leu Leu Lys
 1555 1560 1565

Cys Phe Glu Arg Glu Ser Phe Leu Lys Gln Val Met His Ile Ile Lys
 1570 1575 1580

Ser Val Asp Lys Lys Phe Phe Gln Val Ile Cys Asn Asp Ala Ile Tyr
 585 1590 1595 1600

Ser Glu Gly Pro Ser Arg Ile Thr Ser Thr Leu Phe Leu Glu Ser Leu
 1605 1610 1615

Val His Leu Gly Thr Leu Val Lys Val Asp Phe Ile Leu Asn Ala Leu
 1620 1625 1630

Ile Lys Asn Asn Ala Leu Leu Leu Leu Val Arg Ser Val Lys Arg Thr
 1635 1640 1645

Asp Ala Met Ile Lys Leu Cys Gln Glu Lys Asn Ser Gly Val Thr Leu
 1650 1655 1660

Asp His Phe Ile Phe Asp Leu Met Ala Phe Lys Ala Thr Leu Tyr Phe
 665 1670 1675 1680

Phe Val Arg Val Ala Lys Ser Lys Asn Gly Ala Leu Gln Leu Ile Gln
 1685 1690 1695

Asn Glu Leu Phe Ser Ile Leu His Gln Ser Lys Phe Leu Gln Ile Asp
 1700 1705 1710

Pro Asp Ile Gly Leu Ser Leu Arg Ile Glu Glu Val Gln Asp His Lys
 1715 1720 1725

Thr Val Asn Val Asn Val Leu Leu Asp Thr Pro Leu Ser Ile Thr Asp
 1730 1735 1740

Leu Val Asp Pro Tyr Lys Leu Arg Ser Glu Asn Thr Ile Ser Tyr Phe
 745 1750 1755 1760

Glu Phe Leu Val Pro Ile Phe Gln Leu Leu Thr Thr Val Leu Leu Ser
 1765 1770 1775

Met Gly Pro Asn Tyr Gln Pro Ala Ile Ile Gln Thr Arg Glu Leu Met
 1780 1785 1790

Lys Ser Val Asn Arg Leu Val Val Gly Val Met Lys Arg Asp Phe Leu
 1795 1800 1805

Val Glu Thr Lys Gln Ile Gly Gln Gly Leu Tyr Lys Glu Glu Ser His
 1810 1815 1820

Glu Leu Val Ser Leu Lys Glu Leu Val Lys Leu Phe Ile Leu Ile Asp
 825 1830 1835 1840

Ser Leu Ala His Tyr Ser Val
 1845

<210> 12
 <211> 575
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Probe

<400> 12
 gtttgggtgac tcaacctacc accaatcgat ttacactctt cataagttct ctagtgtgaa 60
 taattgcagg ttgataattht ggtcccattg acaataacac tgttgtaagt agctgaaata 120
 ttggtacaag gaactcaaaa tatgatatag tgttttctact tcgcaacttg tatggatcca 180
 ccaagtcagt tatcgaaagt ggagtatcta gcaaaacatt tacattgaca gtcttgtgat 240
 cttgaacttc ttcaattcgt aaacttaaac caatatctgg atcaatctgc aaaaacttcg 300
 actgatgcaa aattgaaaac aattcatttt ggaatcannn nnanaantna aaaaaaatat 360
 atattntntt tttttttttt ttntttnttt tttattttat cttacannac accccaacac 420
 aacaccaaac ccnaaaacac ccaacacctc catcttgtcc cgcttttctc tcacattttt 480
 tctctactac tatcacacaa tctataaaac atacaccccc tcaaccctc ctccccaaca 540
 aacctacctc cctcaactcc tatttcctcc cttcc 575

<210> 13
 <211> 921
 <212> DNA
 <213> Candida albicans

<220>
 <221> CDS
 <222> (1)..(918)

<220>
 <221> gene
 <222> (1)..(918)
 <223> gene CaOR110

<400> 13
 atg acg att gaa act att tat atc gca aga cac ggt tat aga tcc aat 48
 Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn
 1 5 10 15
 tgg tta cca cca cca cac cca cca aat cct act ggt att gac agt gac 96
 Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp
 20 25 30
 ccg gct tta gca cca cat ggt gtt gaa caa gcc caa cag tta gct gcc 144
 Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala

35	40	45	
tat ctt aca tca tta cct aca cat gaa aag cct gaa ttt att att gct	192		
Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala			
50 55 60			
tca cct ttt tat cgt tgt ata gaa acg tcg aga ccc att gcc gaa atg	240		
Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met			
65 70 75 80			
ttg gac ttg aag att gct tta gaa aga gga gtt ggt gaa tgg ttt cgt	288		
Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg			
85 90 95			
aaa aat aga gat acc aaa cca gtt ccc ggt gat tac aca caa ttg aga	336		
Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg			
100 105 110			
aca ttt ttc gat aaa tta ttg atc gat gaa gat act tgg cca aga gat	384		
Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp			
115 120 125			
aac tta aat gtt ata cct aat att gaa gga gaa gat tat gat gaa atc	432		
Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile			
130 135 140			
tac gat cgt gcc aaa ttg ttt tgg aaa aag ttt att cct gaa ttt gaa	480		
Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu			
145 150 155 160			
aag aaa ttc ccc gaa att aaa aat gtg ttg ata gtt aca cat gca gca	528		
Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala			
165 170 175			
acg aaa att gct tta gga tca gct tta tta cag tta aaa tca gtt act	576		
Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr			
180 185 190			
gat gtt ata gat gat aat caa act gtg tta cgt gct ggt gca tgt tca	624		
Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser			
195 200 205			
tta tcc aaa ttt gtt aga gat ggc gaa gat aaa acc aat cat act att	672		
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile			
210 215 220			
caa tgg aaa att gtc atg aat ggt aat tgt gaa ttc ttg aca cag ggt	720		
Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly			
225 230 235 240			
gaa gaa atg aac tgg gat ttc cgt cgt ggt gtt gaa gcc ggg tca gct	768		
Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala			
245 250 255			
gaa gat ata gcg caa aga aag gca gca gca gaa gca gaa gca aaa gca	816		
Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala			
260 265 270			

ttg aag aaa aat gaa caa acc aaa tcc gat ggt ccc atc act gaa tct 864
 Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser
 275 280 285

gcc act ggg gca gaa ata gat ggg aat gaa gat gaa ttt gaa gta cgt 912
 Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Val Arg
 290 295 300

aaa act tga 921
 Lys Thr
 305

<210> 14
 <211> 306
 <212> PRT
 <213> Candida albicans

<400> 14
 Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn
 1 5 10 15
 Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp
 20 25 30
 Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala
 35 40 45
 Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala
 50 55 60
 Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met
 65 70 75 80
 Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg
 85 90 95
 Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg
 100 105 110
 Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp
 115 120 125
 Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile
 130 135 140
 Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu
 145 150 155 160
 Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala
 165 170 175
 Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr
 180 185 190
 Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser

195 200 205
 Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile
 210 215 220
 Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly
 225 230 235 240
 Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala
 245 250 255
 Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala
 260 265 270
 Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser
 275 280 285
 Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Val Arg
 290 295 300
 Lys Thr
 305

<210> 15
 <211> 1454
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Splice Variant

<220>
 <221> CDS
 <222> (1)..(1452)
 <223> gene CaOR110 Splice Variant

<400> 15
 atg acg att gaa act att tat atc gca aga cac ggt tat aga tcc aat 48
 Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn
 1 5 10 15
 tgg tta cca cca cca cac cca cca aat cct act ggt att gac agt gac 96
 Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp
 20 25 30
 ccg gct tta gca cca cat ggt gtt gaa caa gcc caa cag tta gct gcc 144
 Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala
 35 40 45
 tat ctt aca tca tta cct aca cat gaa aag cct gaa ttt att att gct 192
 Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala
 50 55 60
 tca cct ttt tat cgt tgt ata gaa acg tcg aga ccc att gcc gaa atg 240
 Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met
 65 70 75 80

ttg gac ttg aag att gct tta gaa aga gga gtt ggt gaa tgg ttt cgt	288
Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg	
85 90 95	
aaa aat aga gat acc aaa cca gtt ccc ggt gat tac aca caa ttg aga	336
Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg	
100 105 110	
aca ttt ttc gat aaa tta ttg atc gat gaa gat act tgg cca aga gat	384
Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp	
115 120 125	
aac tta aat gtt ata cct aat att gaa gga gaa gat tat gat gaa atc	432
Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile	
130 135 140	
tac gat cgt gcc aaa ttg ttt tgg aaa aag ttt att cct gaa ttt gaa	480
Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu	
145 150 155 160	
aag aaa ttc ccc gaa att aaa aat gtg ttg ata gtt aca cat gca gca	528
Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala	
165 170 175	
acg aaa att gct tta gga tca gct tta tta cag tta aaa tca gtt act	576
Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr	
180 185 190	
gat gtt ata gat gat aat caa act gtg tta cgt gct ggt gca tgt tca	624
Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser	
195 200 205	
tta tcc aaa ttt gtt aga gat ggc gaa gat aaa acc aat cat act att	672
Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile	
210 215 220	
caa tgg aaa att gtc atg aat ggt aat tgt gaa ttc ttg aca cag ggt	720
Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly	
225 230 235 240	
gaa gaa atg aac tgg gat ttc cgt cgt ggt gtt gaa gcc ggg tca gct	768
Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala	
245 250 255	
gaa gat ata gcg caa aga aag gca gca gca gaa gca gaa gca aaa gca	816
Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala	
260 265 270	
ttg aag aaa aat gaa caa acc aaa tcc gat ggt ccc atc act gaa tct	864
Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser	
275 280 285	
gcc act ggg gca gaa ata gat ggg aat gaa gat gaa ttt gaa aca ttt	912
Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Thr Phe	
290 295 300	

tat gta acc atc gat ata cct tca att tcg aat aaa atc gac aat gaa	960
Tyr Val Thr Ile Asp Ile Pro Ser Ile Ser Asn Lys Ile Asp Asn Glu	
305 310 315 320	
gaa gaa cca cca tca agg aca ggt caa gct cca aaa ttc aaa aac aat	1008
Glu Glu Pro Pro Ser Arg Thr Gly Gln Ala Pro Lys Phe Lys Asn Asn	
325 330 335	
att atc aag cct tca gca caa ctc caa ttt act gat tta aaa gaa gat	1056
Ile Ile Lys Pro Ser Ala Gln Leu Gln Phe Thr Asp Leu Lys Glu Asp	
340 345 350	
cat cca tta gta aaa ata tcg aac aat act ata tct gct caa ggc tcg	1104
His Pro Leu Val Lys Ile Ser Asn Asn Thr Ile Ser Ala Gln Gly Ser	
355 360 365	
tcg tcg tcg tcg tta tca gcg tcg aaa aat gga ttt aat agt cat act	1152
Ser Ser Ser Ser Leu Ser Ala Ser Lys Asn Gly Phe Asn Ser His Thr	
370 375 380	
cac aat tca gga gtc att gat cca tca gca ctt ata gat ggg aaa att	1200
His Asn Ser Gly Val Ile Asp Pro Ser Ala Leu Ile Asp Gly Lys Ile	
385 390 395 400	
tat cag act gat tgg aat caa tta caa ggt act gaa cta ata ttt gat	1248
Tyr Gln Thr Asp Trp Asn Gln Leu Gln Gly Thr Glu Leu Ile Phe Asp	
405 410 415	
gaa aat ggt caa ttt ata ggc aag gtt aag gaa cat ttg act tgc aat	1296
Glu Asn Gly Gln Phe Ile Gly Lys Val Lys Glu His Leu Thr Cys Asn	
420 425 430	
aat aac aca aaa ttc aca tta aaa aag gca gaa gaa gta gaa caa ctt	1344
Asn Asn Thr Lys Phe Thr Leu Lys Lys Ala Glu Glu Val Glu Gln Leu	
435 440 445	
cgt tca gca gat gat tct atc atg gat ata gat caa gac tca caa gga	1392
Arg Ser Ala Asp Asp Ser Ile Met Asp Ile Asp Gln Asp Ser Gln Gly	
450 455 460	
caa caa cca gct aga agt cag ttc tta aaa aga gca att gtg gct gct	1440
Gln Gln Pro Ala Arg Ser Gln Phe Leu Lys Arg Ala Ile Val Ala Ala	
465 470 475 480	
aga gcc aaa ggt aa	1454
Arg Ala Lys Gly	

<210> 16

<211> 484

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Splice Variant

<400> 16

Met Thr Ile Glu Thr Ile Tyr Ile Ala Arg His Gly Tyr Arg Ser Asn
1 5 10 15

Trp Leu Pro Pro Pro His Pro Pro Asn Pro Thr Gly Ile Asp Ser Asp
 20 25 30
 Pro Ala Leu Ala Pro His Gly Val Glu Gln Ala Gln Gln Leu Ala Ala
 35 40 45
 Tyr Leu Thr Ser Leu Pro Thr His Glu Lys Pro Glu Phe Ile Ile Ala
 50 55 60
 Ser Pro Phe Tyr Arg Cys Ile Glu Thr Ser Arg Pro Ile Ala Glu Met
 65 70 75 80
 Leu Asp Leu Lys Ile Ala Leu Glu Arg Gly Val Gly Glu Trp Phe Arg
 85 90 95
 Lys Asn Arg Asp Thr Lys Pro Val Pro Gly Asp Tyr Thr Gln Leu Arg
 100 105 110
 Thr Phe Phe Asp Lys Leu Leu Ile Asp Glu Asp Thr Trp Pro Arg Asp
 115 120 125
 Asn Leu Asn Val Ile Pro Asn Ile Glu Gly Glu Asp Tyr Asp Glu Ile
 130 135 140
 Tyr Asp Arg Ala Lys Leu Phe Trp Lys Lys Phe Ile Pro Glu Phe Glu
 145 150 155 160
 Lys Lys Phe Pro Glu Ile Lys Asn Val Leu Ile Val Thr His Ala Ala
 165 170 175
 Thr Lys Ile Ala Leu Gly Ser Ala Leu Leu Gln Leu Lys Ser Val Thr
 180 185 190
 Asp Val Ile Asp Asp Asn Gln Thr Val Leu Arg Ala Gly Ala Cys Ser
 195 200 205
 Leu Ser Lys Phe Val Arg Asp Gly Glu Asp Lys Thr Asn His Thr Ile
 210 215 220
 Gln Trp Lys Ile Val Met Asn Gly Asn Cys Glu Phe Leu Thr Gln Gly
 225 230 235 240
 Glu Glu Met Asn Trp Asp Phe Arg Arg Gly Val Glu Ala Gly Ser Ala
 245 250 255
 Glu Asp Ile Ala Gln Arg Lys Ala Ala Ala Glu Ala Glu Ala Lys Ala
 260 265 270
 Leu Lys Lys Asn Glu Gln Thr Lys Ser Asp Gly Pro Ile Thr Glu Ser
 275 280 285
 Ala Thr Gly Ala Glu Ile Asp Gly Asn Glu Asp Glu Phe Glu Thr Phe
 290 295 300
 Tyr Val Thr Ile Asp Ile Pro Ser Ile Ser Asn Lys Ile Asp Asn Glu
 305 310 315 320

Glu Glu Pro Pro Ser Arg Thr Gly Gln Ala Pro Lys Phe Lys Asn Asn
 325 330 335
 Ile Ile Lys Pro Ser Ala Gln Leu Gln Phe Thr Asp Leu Lys Glu Asp
 340 345 350
 His Pro Leu Val Lys Ile Ser Asn Asn Thr Ile Ser Ala Gln Gly Ser
 355 360 365
 Ser Ser Ser Ser Leu Ser Ala Ser Lys Asn Gly Phe Asn Ser His Thr
 370 375 380
 His Asn Ser Gly Val Ile Asp Pro Ser Ala Leu Ile Asp Gly Lys Ile
 385 390 395 400
 Tyr Gln Thr Asp Trp Asn Gln Leu Gln Gly Thr Glu Leu Ile Phe Asp
 405 410 415
 Glu Asn Gly Gln Phe Ile Gly Lys Val Lys Glu His Leu Thr Cys Asn
 420 425 430
 Asn Asn Thr Lys Phe Thr Leu Lys Lys Ala Glu Glu Val Glu Gln Leu
 435 440 445
 Arg Ser Ala Asp Asp Ser Ile Met Asp Ile Asp Gln Asp Ser Gln Gly
 450 455 460
 Gln Gln Pro Ala Arg Ser Gln Phe Leu Lys Arg Ala Ile Val Ala Ala
 465 470 475 480
 Arg Ala Lys Gly

<210> 17
 <211> 2877
 <212> DNA
 <213> Candida albicans

<220>
 <221> CDS
 <222> (1)..(2874)

<220>
 <221> gene
 <222> (1)..(2874)
 <223> gene CaMR212

<400> 17
 atg aat ttg ttt caa cat aaa cat caa aaa tta ata tta caa tgt tat 48
 Met Asn Leu Phe Gln His Lys His Gln Lys Leu Ile Leu Gln Cys Tyr
 1 5 10 15
 cct gct ggg aaa gca gtg gac aaa aaa ccc aac tcg tcc gag tta agt 96
 Pro Ala Gly Lys Ala Val Asp Lys Lys Pro Asn Ser Ser Glu Leu Ser
 20 25 30

tat tta tta tac tat gca tcc act cgt aga gtc aaa tta gaa aag gtg	144
Tyr Leu Leu Tyr Tyr Ala Ser Thr Arg Arg Val Lys Leu Glu Lys Val	
35 40 45	
att aat ttt ttg aaa gat aaa act cat cat gat gtt ggt aga aac cgt	192
Ile Asn Phe Leu Lys Asp Lys Thr His His Asp Val Gly Arg Asn Arg	
50 55 60	
act ggt aat tta caa gtc aca tta gcc att att cag gaa tta atc aaa	240
Thr Gly Asn Leu Gln Val Thr Leu Ala Ile Ile Gln Glu Leu Ile Lys	
65 70 75 80	
aaa tgt agt gaa aac ttg aat gtt ttt gcc ttt caa gtg tgc tat atc	288
Lys Cys Ser Glu Asn Leu Asn Val Phe Ala Phe Gln Val Cys Tyr Ile	
85 90 95	
ttg caa ctg att gcc aac act aag gat ctt gcc ttg tgt aaa aat gtt	336
Leu Gln Leu Ile Ala Asn Thr Lys Asp Leu Ala Leu Cys Lys Asn Val	
100 105 110	
gtc aaa aca ttt ggt gtt ttg tgt gaa aac ttg gat ggt ggg ttg ttc	384
Val Lys Thr Phe Gly Val Leu Cys Glu Asn Leu Asp Gly Gly Leu Phe	
115 120 125	
aca ggt gat aag gag ttt ata aag att ttc act gaa gtt ttc caa aca	432
Thr Gly Asp Lys Glu Phe Ile Lys Ile Phe Thr Glu Val Phe Gln Thr	
130 135 140	
tta gtt tcc ttt ggt aag gac aga tcg ggt gtt act cag tat gat tgg	480
Leu Val Ser Phe Gly Lys Asp Arg Ser Gly Val Thr Gln Tyr Asp Trp	
145 150 155 160	
cag atg att tct tta atg gct ata aat gat ata tcc agt tgt ttg agt	528
Gln Met Ile Ser Leu Met Ala Ile Asn Asp Ile Ser Ser Cys Leu Ser	
165 170 175	
tat aat gca gct gtt ggt aaa aag ttt att gct ttg tcg att cct gtt	576
Tyr Asn Ala Ala Val Gly Lys Lys Phe Ile Ala Leu Ser Ile Pro Val	
180 185 190	
tta ctt cag ttt att att gca aac aac cca caa agc agc ata ttg caa	624
Leu Leu Gln Phe Ile Ile Ala Asn Asn Pro Gln Ser Ser Ile Leu Gln	
195 200 205	
aga ttg aaa tcg aat ctc cac gtt gaa gat gat ggg aag agg ttg tca	672
Arg Leu Lys Ser Asn Leu His Val Glu Asp Asp Gly Lys Arg Leu Ser	
210 215 220	
cgt gct cat ctg caa aaa tcc cat agc aaa att gcc caa caa att gat	720
Arg Ala His Leu Gln Lys Ser His Ser Lys Ile Ala Gln Gln Ile Asp	
225 230 235 240	
gat gat ttc acc aat gat tct tta acc ttg aca gat atc act gaa aag	768
Asp Asp Phe Thr Asn Asp Ser Leu Thr Leu Thr Asp Ile Thr Glu Lys	
245 250 255	
gca ttt tcg tcg atg aaa tct ttt ttc aat acc aat gct gcc agt caa	816

Ala	Phe	Ser	Ser	Met	Lys	Ser	Phe	Phe	Asn	Thr	Asn	Ala	Ala	Ser	Gln	
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Ile	Ser	Glu	Val	Thr	Arg	Ala	Val	Val	Gln	His	Asn	Ile	Leu	Asn	Gly	
		275					280				285					
acc	gat	ttg	gag	tggt	gga	gtc	tca	ttc	ttg	gaa	tta	tgt	att	act	tggt	912
Thr	Asp	Leu	Glu	Trp	Gly	Val	Ser	Phe	Leu	Glu	Leu	Cys	Ile	Thr	Trp	
	290					295					300					
att	cca	gtt	caa	tta	cgt	ttt	gtc	agt	ttg	tcc	acc	ttg	ttg	gcc	act	960
Ile	Pro	Val	Gln	Leu	Arg	Phe	Val	Ser	Leu	Ser	Thr	Leu	Leu	Ala	Thr	
305					310				315						320	
tta	ggt	aga	att	aat	att	gaa	ggt	aac	acc	aaa	tcc	aat	tac	aac	atg	1008
Leu	Gly	Arg	Ile	Asn	Ile	Glu	Gly	Asn	Thr	Lys	Ser	Asn	Tyr	Asn	Met	
			325					330						335		
caa	ttc	cag	tat	gct	cgt	tac	ttg	tta	gga	tta	ctt	tca	tct	cgt	gtg	1056
Gln	Phe	Gln	Tyr	Ala	Arg	Tyr	Leu	Leu	Gly	Leu	Leu	Ser	Ser	Arg	Val	
			340					345					350			
aac	atg	att	ggg	tta	tca	gtt	tca	gat	att	att	caa	cag	ttg	tta	tcg	1104
Asn	Met	Ile	Gly	Leu	Ser	Val	Ser	Asp	Ile	Ile	Gln	Gln	Leu	Leu	Ser	
		355					360					365				
ttg	caa	gct	gat	ttg	att	ttg	aag	gca	agt	gat	ttg	gac	aaa	agt	gaa	1152
Leu	Gln	Ala	Asp	Leu	Ile	Leu	Lys	Ala	Ser	Asp	Leu	Asp	Lys	Ser	Glu	
	370					375					380					
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Ile	Ser	Ile	Leu	Thr	Asp	Ile	Tyr	Ser	Asp	Cys	Ile	Cys	Ser	Leu	Thr	
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Thr	His	Ile	Tyr	Tyr	Phe	Asp	Gln	Val	Pro	Asp	Ser	Ile	Gln	Glu	Ile	
			405						410					415		
tta	atc	aag	att	gat	tac	att	tta	gaa	agc	agt	ttt	gtg	gaa	gat	aat	1296
Leu	Ile	Lys	Ile	Asp	Tyr	Ile	Leu	Glu	Ser	Ser	Phe	Val	Glu	Asp	Asn	
		420						425					430			
aac	att	acg	tcc	act	gga	gaa	caa	att	caa	gat	ttg	att	atc	caa	ttg	1344
Asn	Ile	Thr	Ser	Thr	Gly	Glu	Gln	Ile	Gln	Asp	Leu	Ile	Ile	Gln	Leu	
		435					440					445				
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Leu	Asp	Asn	Ile	Ser	Lys	Ile	Phe	Leu	Ile	Leu	Lys	Asn	Lys	Ser	Ser	
	450					455					460					
tca	att	aat	cgt	aac	cat	gtg	aat	ttg	gaa	cat	tggt	gat	atc	agt	tta	1440
Ser	Ile	Asn	Arg	Asn	His	Val	Asn	Leu	Glu	His	Trp	Asp	Ile	Ser	Leu	
465					470					475					480	
gga	tta	ttg	gct	cca	caa	ggc	gac	cat	gat	gat	aac	aga	aaa	atg	att	1488
Gly	Leu	Leu	Ala	Pro	Gln	Gly	Asp	His	Asp	Asp	Asn	Arg	Lys	Met	Ile	

485										490					495					
att tct acg aca caa ctt atc aat atc caa gcc agg tac ttg aaa gtg	1536																			
Ile Ser Thr Thr Gln Leu Ile Asn Ile Gln Ala Arg Tyr Leu Lys Val																				
500 505 510																				
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Phe Asp Glu Phe Leu Asn Asn Glu Leu Ala Val Gly Asn Ser Lys Lys																				
515 520 525																				
agc tat gat ctt ctt agc aaa cag tct cgt ttg gat cct gga agt aca	1632																			
Ser Tyr Asp Leu Leu Ser Lys Gln Ser Arg Leu Asp Pro Gly Ser Thr																				
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gct gtt gaa gga gtg aac aag tct gac gat ctg gac aat ggt aag gac	1680																			
Ala Val Glu Gly Val Asn Lys Ser Asp Asp Leu Asp Asn Gly Lys Asp																				
545 550 555 560																				
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Phe Lys Lys Pro Asp Ala Asn Gln Tyr Ile Thr Asn Gln Gln Asn Phe																				
565 570 575																				
ata tcc cat ttc ctt atg tat atc gac aaa ttt ttc gaa aat tac gat	1776																			
Ile Ser His Phe Leu Met Tyr Ile Asp Lys Phe Phe Glu Asn Tyr Asp																				
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Ser Pro Asn Thr Gln Ser Val Leu Leu Val Thr Val Leu Lys Asp																				
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Met Met Asn Ile Leu Gly Leu Asn Phe Leu Ser Asn Phe Ile Pro Phe																				
610 615 620																				
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Phe His His Trp Val Met Lys Val Asn Arg Ala Ser Asn Phe Thr Gln																				
625 630 635 640																				
aga cag aaa ttc aaa gat act ttt gct cat att att tta tat tac atg	1968																			
Arg Gln Lys Phe Lys Asp Thr Phe Ala His Ile Ile Leu Tyr Tyr Met																				
645 650 655																				
ttg aaa gat ttg gat gag caa tat agt cat gat tta caa aat tat tgc	2016																			
Leu Lys Asp Leu Asp Glu Gln Tyr Ser His Asp Leu Gln Asn Tyr Cys																				
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aaa agc tct aaa tta ttc aaa caa ata ttg gat gct gtt gaa tat aga	2064																			
Lys Ser Ser Lys Leu Phe Lys Gln Ile Leu Asp Ala Val Glu Tyr Arg																				
675 680 685																				
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Lys Met Gln Lys Phe Trp Val His Gly Ile Asp Pro Ser Pro Ser Asp																				
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Leu Glu Asn Thr Lys Gly Asp Arg Thr Ile Pro Thr Asp Ala Asn Gly																				
705 710 715 720																				

aat tat att gct att aga atc aaa cct gaa aat att gag gaa ttt gcc	2208
Asn Tyr Ile Ala Ile Arg Ile Lys Pro Glu Asn Ile Glu Glu Phe Ala	
725 730 735	
tgt ggt aac aac ttt ttg att gta tgg tta cat ccc caa aaa caa tta	2256
Cys Gly Asn Asn Phe Leu Ile Val Trp Leu His Pro Gln Lys Gln Leu	
740 745 750	
ctc act gaa att gaa aaa tca caa gtc agt act cat atg agc aca ttc	2304
Leu Thr Glu Ile Glu Lys Ser Gln Val Ser Thr His Met Ser Thr Phe	
755 760 765	
aat aat gat tct aga aac aca aat atg aca gtg ata atg gat caa gga	2352
Asn Asn Asp Ser Arg Asn Thr Asn Met Thr Val Ile Met Asp Gln Gly	
770 775 780	
tca ctg gca cta agt gga ggt gca gac cat gga ggt cac ttt gtt ccg	2400
Ser Leu Ala Leu Ser Gly Gly Ala Asp His Gly Gly His Phe Val Pro	
785 790 795 800	
cca cct gaa ttt gtt aac cac acc ggt ttg tct tct gaa tct gcg tca	2448
Pro Pro Glu Phe Val Asn His Thr Gly Leu Ser Ser Glu Ser Ala Ser	
805 810 815	
tca aac tca gag aaa ggt ttg tat act ggt tta gga ttg ggt act gct	2496
Ser Asn Ser Glu Lys Gly Leu Tyr Thr Gly Leu Gly Leu Gly Thr Ala	
820 825 830	
ggt gat att act atg att cat tct gaa ata tta caa tac agt caa cat	2544
Gly Asp Ile Thr Met Ile His Ser Glu Ile Leu Gln Tyr Ser Gln His	
835 840 845	
ttc caa gaa aga ggt tta cct cat ggt aat ggg ttt gct act att tta	2592
Phe Gln Glu Arg Gly Leu Pro His Gly Asn Gly Phe Ala Thr Ile Leu	
850 855 860	
cga act gtc gat agt gtt aac agt act aat gat ggg tta att tat act	2640
Arg Thr Val Asp Ser Val Asn Ser Thr Asn Asp Gly Leu Ile Tyr Thr	
865 870 875 880	
tat gat agt aaa tat ttg cag tca cca aga gta agt gat ttg aaa gat	2688
Tyr Asp Ser Lys Tyr Leu Gln Ser Pro Arg Val Ser Asp Leu Lys Asp	
885 890 895	
gcc atg tca aca cat agg ggt ata agg tta tct aaa cca aat ttt ggt	2736
Ala Met Ser Thr His Arg Gly Ile Arg Leu Ser Lys Pro Asn Phe Gly	
900 905 910	
ggt gcc aat gga act gct aat atg acg gat tct gct tct aca tcc aat	2784
Gly Ala Asn Gly Thr Ala Asn Met Thr Asp Ser Ala Ser Thr Ser Asn	
915 920 925	
gga tct gtg ttg aat aaa aat atg caa act aca gat gtt gat tca att	2832
Gly Ser Val Leu Asn Lys Asn Met Gln Thr Thr Asp Val Asp Ser Ile	
930 935 940	

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 945 950 955

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 35 40 45
 Ile Asn Phe Leu Lys Asp Lys Thr His His Asp Val Gly Arg Asn Arg
 50 55 60
 Thr Gly Asn Leu Gln Val Thr Leu Ala Ile Ile Gln Glu Leu Ile Lys
 65 70 75 80
 Lys Cys Ser Glu Asn Leu Asn Val Phe Ala Phe Gln Val Cys Tyr Ile
 85 90 95
 Leu Gln Leu Ile Ala Asn Thr Lys Asp Leu Ala Leu Cys Lys Asn Val
 100 105 110
 Val Lys Thr Phe Gly Val Leu Cys Glu Asn Leu Asp Gly Gly Leu Phe
 115 120 125
 Thr Gly Asp Lys Glu Phe Ile Lys Ile Phe Thr Glu Val Phe Gln Thr
 130 135 140
 Leu Val Ser Phe Gly Lys Asp Arg Ser Gly Val Thr Gln Tyr Asp Trp
 145 150 155 160
 Gln Met Ile Ser Leu Met Ala Ile Asn Asp Ile Ser Ser Cys Leu Ser
 165 170 175
 Tyr Asn Ala Ala Val Gly Lys Lys Phe Ile Ala Leu Ser Ile Pro Val
 180 185 190
 Leu Leu Gln Phe Ile Ile Ala Asn Asn Pro Gln Ser Ser Ile Leu Gln
 195 200 205
 Arg Leu Lys Ser Asn Leu His Val Glu Asp Asp Gly Lys Arg Leu Ser
 210 215 220
 Arg Ala His Leu Gln Lys Ser His Ser Lys Ile Ala Gln Gln Ile Asp
 225 230 235 240
 Asp Asp Phe Thr Asn Asp Ser Leu Thr Leu Thr Asp Ile Thr Glu Lys

245	250	255
Ala Phe Ser Ser Met Lys Ser Phe Phe Asn Thr Asn Ala Ala Ser Gln		
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275	280	285
Thr Asp Leu Glu Trp Gly Val Ser Phe Leu Glu Leu Cys Ile Thr Trp		
290	295	300
Ile Pro Val Gln Leu Arg Phe Val Ser Leu Ser Thr Leu Leu Ala Thr		
305	310	315
Leu Gly Arg Ile Asn Ile Glu Gly Asn Thr Lys Ser Asn Tyr Asn Met		
325	330	335
Gln Phe Gln Tyr Ala Arg Tyr Leu Leu Gly Leu Leu Ser Ser Arg Val		
340	345	350
Asn Met Ile Gly Leu Ser Val Ser Asp Ile Ile Gln Gln Leu Leu Ser		
355	360	365
Leu Gln Ala Asp Leu Ile Leu Lys Ala Ser Asp Leu Asp Lys Ser Glu		
370	375	380
Ile Ser Ile Leu Thr Asp Ile Tyr Ser Asp Cys Ile Cys Ser Leu Thr		
385	390	395
Thr His Ile Tyr Tyr Phe Asp Gln Val Pro Asp Ser Ile Gln Glu Ile		
405	410	415
Leu Ile Lys Ile Asp Tyr Ile Leu Glu Ser Ser Phe Val Glu Asp Asn		
420	425	430
Asn Ile Thr Ser Thr Gly Glu Gln Ile Gln Asp Leu Ile Ile Gln Leu		
435	440	445
Leu Asp Asn Ile Ser Lys Ile Phe Leu Ile Leu Lys Asn Lys Ser Ser		
450	455	460
Ser Ile Asn Arg Asn His Val Asn Leu Glu His Trp Asp Ile Ser Leu		
465	470	475
Gly Leu Leu Ala Pro Gln Gly Asp His Asp Asp Asn Arg Lys Met Ile		
485	490	495
Ile Ser Thr Thr Gln Leu Ile Asn Ile Gln Ala Arg Tyr Leu Lys Val		
500	505	510
Phe Asp Glu Phe Leu Asn Asn Glu Leu Ala Val Gly Asn Ser Lys Lys		
515	520	525
Ser Tyr Asp Leu Leu Ser Lys Gln Ser Arg Leu Asp Pro Gly Ser Thr		
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Ala Val Glu Gly Val Asn Lys Ser Asp Asp Leu Asp Asn Gly Lys Asp		

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Phe Lys Lys Pro Asp Ala Asn Gln Tyr Ile Thr Asn Gln Gln Asn Phe						
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Ile Ser His Phe Leu Met Tyr Ile Asp Lys Phe Phe Glu Asn Tyr Asp						
		580		585		590
Ser Pro Asn Thr Gln Ser Val Leu Leu Leu Val Thr Val Leu Lys Asp						
		595		600		605
Met Met Asn Ile Leu Gly Leu Asn Phe Leu Ser Asn Phe Ile Pro Phe						
		610		615		620
Phe His His Trp Val Met Lys Val Asn Arg Ala Ser Asn Phe Thr Gln						
		625		630		635
Arg Gln Lys Phe Lys Asp Thr Phe Ala His Ile Ile Leu Tyr Tyr Met						
		645		650		655
Leu Lys Asp Leu Asp Glu Gln Tyr Ser His Asp Leu Gln Asn Tyr Cys						
		660		665		670
Lys Ser Ser Lys Leu Phe Lys Gln Ile Leu Asp Ala Val Glu Tyr Arg						
		675		680		685
Lys Met Gln Lys Phe Trp Val His Gly Ile Asp Pro Ser Pro Ser Asp						
		690		695		700
Leu Glu Asn Thr Lys Gly Asp Arg Thr Ile Pro Thr Asp Ala Asn Gly						
		705		710		715
Asn Tyr Ile Ala Ile Arg Ile Lys Pro Glu Asn Ile Glu Glu Phe Ala						
		725		730		735
Cys Gly Asn Asn Phe Leu Ile Val Trp Leu His Pro Gln Lys Gln Leu						
		740		745		750
Leu Thr Glu Ile Glu Lys Ser Gln Val Ser Thr His Met Ser Thr Phe						
		755		760		765
Asn Asn Asp Ser Arg Asn Thr Asn Met Thr Val Ile Met Asp Gln Gly						
		770		775		780
Ser Leu Ala Leu Ser Gly Gly Ala Asp His Gly Gly His Phe Val Pro						
		785		790		795
Pro Pro Glu Phe Val Asn His Thr Gly Leu Ser Ser Glu Ser Ala Ser						
		805		810		815
Ser Asn Ser Glu Lys Gly Leu Tyr Thr Gly Leu Gly Leu Gly Thr Ala						
		820		825		830
Gly Asp Ile Thr Met Ile His Ser Glu Ile Leu Gln Tyr Ser Gln His						
		835		840		845
Phe Gln Glu Arg Gly Leu Pro His Gly Asn Gly Phe Ala Thr Ile Leu						

850 855 860
 Arg Thr Val Asp Ser Val Asn Ser Thr Asn Asp Gly Leu Ile Tyr Thr
 865 870 875 880
 Tyr Asp Ser Lys Tyr Leu Gln Ser Pro Arg Val Ser Asp Leu Lys Asp
 885 890 895
 Ala Met Ser Thr His Arg Gly Ile Arg Leu Ser Lys Pro Asn Phe Gly
 900 905 910
 Gly Ala Asn Gly Thr Ala Asn Met Thr Asp Ser Ala Ser Thr Ser Asn
 915 920 925
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 aaaggcaaaa acattcaagt ttctactaca ttttttgatt aattcctgaa taatggctaa 180
 tgtgacttgt aaattaccag tacggtttct accaacatca tgatgagttt tatctttcaa 240
 aaaattaatc accttttcta atttgactct acgagtggat gcatagtata ataaataact 300
 taactcggac gagttgggtt ttttgtccac tgctttccca gcaggataac attgtaatat 360
 taacttttga tgtttatggt gaaacaaatt cattcttgga tctggaagtt gaagaaacta 420
 ttgaatcaaa acaggattta attaaccaat agaaaagaag taactcttga gttaaaaagg 480
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act ttg gat gaa ata aaa tat gcc atg aaa cat gtt ttc caa gat gct 96
 Thr Leu Asp Glu Ile Lys Tyr Ala Met Lys His Val Phe Gln Asp Ala
 20 25 30

caa tta ggt tta gca gga cat aga aaa tta gtg gta att ttg aaa aat 144
 Gln Leu Gly Leu Ala Gly His Arg Lys Leu Val Val Ile Leu Lys Asn
 35 40 45

gta ttt aaa aaa gcc att gaa tta aat caa att aat ttc ttt gcc atg 192
 Val Phe Lys Lys Ala Ile Glu Leu Asn Gln Ile Asn Phe Phe Ala Met
 50 55 60

tgt ttt act aaa ttg tta tct aaa gta tta cct ttg aaa aga gga gtt 240
 Cys Phe Thr Lys Leu Leu Ser Lys Val Leu Pro Leu Lys Arg Gly Val
 65 70 75 80

ttg gca ggt gat aga ata gtc aaa ttt tgt tat ctg ttt gtt aat ggt 288
 Leu Ala Gly Asp Arg Ile Val Lys Phe Cys Tyr Leu Phe Val Asn Gly
 85 90 95

ctt gta aaa gat gcc aat gaa gaa aaa cgt tcc aaa gaa gaa gaa aaa 336
 Leu Val Lys Asp Ala Asn Glu Glu Lys Arg Ser Lys Glu Glu Glu Lys
 100 105 110

gaa gaa aaa gac aaa gac gaa gac aaa gat acg aat gaa agt gat aaa 384
 Glu Glu Lys Asp Lys Asp Glu Asp Lys Asp Thr Asn Glu Ser Asp Lys
 115 120 125

aat gaa gaa gat cag gaa gat caa gaa gga gaa gga gat caa gaa act 432
 Asn Glu Glu Asp Gln Glu Asp Gln Glu Gly Glu Gly Asp Gln Glu Thr
 130 135 140

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 Pro Ile Ser Glu Phe Ile Ser Tyr Leu Ile Lys Tyr Leu Leu Ser Gly
 145 150 155 160

ata gag gct aaa gat aaa ctg gtt cgt tat cgt gtt gta caa aca tta 528
 Ile Glu Ala Lys Asp Lys Leu Val Arg Tyr Arg Val Val Gln Thr Leu
 165 170 175

gca tac ttg gtt gaa ttc ttg acc gag ata cac gag aat aat aca ttg 576
 Ala Tyr Leu Val Glu Phe Leu Thr Glu Ile His Glu Asn Asn Thr Leu
 180 185 190

gaa gcg tta tat act tta tta agt aat agg cta caa gat aaa gag ctg	624
Glu Ala Leu Tyr Thr Leu Leu Ser Asn Arg Leu Gln Asp Lys Glu Leu	
195 200 205	
tcg ata cgt att caa gct gtt gtg gca tta tca cat ttt caa tta ttt	672
Ser Ile Arg Ile Gln Ala Val Val Ala Leu Ser His Phe Gln Leu Phe	
210 215 220	
gaa ttt agt att gaa ggt gat act gga gaa ttt gag gat gaa tta ata	720
Glu Phe Ser Ile Glu Gly Asp Thr Gly Glu Phe Glu Asp Glu Leu Ile	
225 230 235 240	
tca agt aac caa att cag aat aaa ttg ata aat tcc att caa aat gat	768
Ser Ser Asn Gln Ile Gln Asn Lys Leu Ile Asn Ser Ile Gln Asn Asp	
245 250 255	
gat agt cca gaa gtc aga cgt gca gca tta atg aat ttg gtt aaa aca	816
Asp Ser Pro Glu Val Arg Arg Ala Ala Leu Met Asn Leu Val Lys Thr	
260 265 270	
caa gat aca ata ccg att tta ctt gaa cga gcc aga gat tcc aat tct	864
Gln Asp Thr Ile Pro Ile Leu Leu Glu Arg Ala Arg Asp Ser Asn Ser	
275 280 285	
att aat aga aga ttg gtt tat tct aaa ata gct cgt gaa tta ata act	912
Ile Asn Arg Arg Leu Val Tyr Ser Lys Ile Ala Arg Glu Leu Ile Thr	
290 295 300	
gat ttg gat gat ctt gaa ttt gaa gat agg gaa ttt tta tta aaa tgg	960
Asp Leu Asp Asp Leu Glu Phe Glu Asp Arg Glu Phe Leu Leu Lys Trp	
305 310 315 320	
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Gly Leu Asn Asp Arg Asp Glu Thr Val Lys Ala Ala Ala Thr Lys Met	
325 330 335	
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Leu Thr Ile Tyr Trp Tyr Gln Ser Val Asn Glu Asp Leu Leu Glu Leu	
340 345 350	
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355 360 365	
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Ala Phe Phe Lys Asn Lys Pro Glu Val Leu Glu Thr Ile Lys Ile Asp	
370 375 380	
gaa tca tat tgg aaa aat cta act aca gaa aag gca ttc ttg atg agg	1200
Glu Ser Tyr Trp Lys Asn Leu Thr Thr Glu Lys Ala Phe Leu Met Arg	
385 390 395 400	
acg ttt tat caa tat tgt aat gag aat caa tta cat gct tta atg gat	1248
Thr Phe Tyr Gln Tyr Cys Asn Glu Asn Gln Leu His Ala Leu Met Asp	
405 410 415	

gcc aat ttc cct gaa tta ctt gat ttg tca ata aca tta gaa aag tat	1296
Ala Asn Phe Pro Glu Leu Leu Asp Leu Ser Ile Thr Leu Glu Lys Tyr	
420 425 430	
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Leu Ser Val Arg Leu Lys Thr Ile Asn Glu Asn Glu Asn Leu Val Lys	
435 440 445	
aca tgg gaa act tat aat gcc aag att gac gaa tta gat gat caa ata	1392
Thr Trp Glu Thr Tyr Asn Ala Lys Ile Asp Glu Leu Asp Asp Gln Ile	
450 455 460	
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Phe Ser Leu Glu Asn Gln Ile Ser Arg Ile Asn Thr Asp Ala Asp Asn	
465 470 475 480	
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Phe Arg Lys Ser Leu Ser Asn Ile Glu Glu Asp Ile Ile Glu Ile Asn	
485 490 495	
att gct aag gat ttg ttc aaa aag aga att aaa caa ttg aaa aac aac	1536
Ile Ala Lys Asp Leu Phe Lys Lys Arg Ile Lys Gln Leu Lys Asn Asn	
500 505 510	
agt ggg aat cta gaa gat ttg att act gaa gaa aat caa gag att gct	1584
Ser Gly Asn Leu Glu Asp Leu Ile Thr Glu Glu Asn Gln Glu Ile Ala	
515 520 525	
gat caa atc aag gat ttc ctg atg gaa gat ttg caa caa caa ttg gaa	1632
Asp Gln Ile Lys Asp Phe Leu Met Glu Asp Leu Gln Gln Gln Leu Glu	
530 535 540	
gat atc aat aaa aat ctt gat gaa att gaa cat cat cca gaa gat ata	1680
Asp Ile Asn Lys Asn Leu Asp Glu Ile Glu His His Pro Glu Asp Ile	
545 550 555 560	
acg gct aaa tta gaa gaa ctt caa aca aaa tat gat tct tgt att agg	1728
Thr Ala Lys Leu Glu Glu Leu Gln Thr Lys Tyr Asp Ser Cys Ile Arg	
565 570 575	
gcg ctt gaa acc act agt gaa ttg aaa att cag act gtt caa atc ttt	1776
Ala Leu Glu Thr Thr Ser Glu Leu Lys Ile Gln Thr Val Gln Ile Phe	
580 585 590	
gaa caa gaa cat gaa aat gat tgt atc ccc ttt gta gat gct ttg aaa	1824
Glu Gln Glu His Glu Asn Asp Cys Ile Pro Phe Val Asp Ala Leu Lys	
595 600 605	
gaa tta gaa ttc att att aat caa tta tta tta att gtt aaa gat ttt	1872
Glu Leu Glu Phe Ile Ile Asn Gln Leu Leu Leu Ile Val Lys Asp Phe	
610 615 620	
gat tat gga gat gaa atg gca aga aga aaa ttg tta cat ata ata aga	1920
Asp Tyr Gly Asp Glu Met Ala Arg Arg Lys Leu Leu His Ile Ile Arg	
625 630 635 640	
atg aca tta act gaa gat aaa tta cct gat gcg tta ata tca gtg gca	1968

Met	Thr	Leu	Thr	Glu	Asp	Lys	Leu	Pro	Asp	Ala	Leu	Ile	Ser	Val	Ala	
				645					650					655		
ctt	aga	gta	tta	cga	gca	ctt	tct	ata	aat	gaa	aaa	gat	ttt	gtt	tcc	2016
Leu	Arg	Val	Leu	Arg	Ala	Leu	Ser	Ile	Asn	Glu	Lys	Asp	Phe	Val	Ser	
			660					665					670			
atg	gcg	gta	gaa	ata	att	act	gat	att	cgt	gat	tct	cga	gat	gat	gaa	2064
Met	Ala	Val	Glu	Ile	Ile	Thr	Asp	Ile	Arg	Asp	Ser	Arg	Asp	Asp	Glu	
		675					680					685				
gag	ttc	cat	tct	gct	gcc	gct	aca	ttt	gat	gat	gat	gat	gat	gat	att	2112
Glu	Phe	His	Ser	Ala	Ala	Ala	Thr	Phe	Asp	Asp	Asp	Asp	Asp	Asp	Ile	
	690					695					700					
ttg	gga	aat	ggg	gat	gat	gaa	tct	caa	caa	tca	tca	tca	ctc	agt	gca	2160
Leu	Gly	Asn	Gly	Asp	Asp	Glu	Ser	Gln	Gln	Ser	Ser	Ser	Leu	Ser	Ala	
705					710					715					720	
gta	aca	aag	aag	cga	aga	att	gaa	cca	gat	atg	cca	cca	gat	gat	att	2208
Val	Thr	Lys	Lys	Arg	Arg	Ile	Glu	Pro	Asp	Met	Pro	Pro	Asp	Asp	Ile	
				725				730					735			
gtg	tta	aga	tgt	ctt	acc	atg	aca	caa	tat	gta	ttg	gaa	gta	att	act	2256
Val	Leu	Arg	Cys	Leu	Thr	Met	Thr	Gln	Tyr	Val	Leu	Glu	Val	Ile	Thr	
			740					745					750			
cat	agt	ttg	gat	gat	cat	ctt	tca	ttg	agt	tct	att	tac	agt	ggg	att	2304
His	Ser	Leu	Asp	Asp	His	Leu	Ser	Leu	Ser	Ser	Ile	Tyr	Ser	Gly	Ile	
		755					760					765				
gtc	aat	tat	gct	att	cag	aat	gaa	tcg	aaa	aag	aaa	tta	tat	ctt	gct	2352
Val	Asn	Tyr	Ala	Ile	Gln	Asn	Glu	Ser	Lys	Lys	Lys	Leu	Tyr	Leu	Ala	
	770					775					780					
ggg	tta	act	tgt	tta	gga	ctt	tat	tct	tta	att	gat	tcc	aaa	att	gcc	2400
Gly	Leu	Thr	Cys	Leu	Gly	Leu	Tyr	Ser	Leu	Ile	Asp	Ser	Lys	Ile	Ala	
785					790					795					800	
aga	att	gca	act	aca	aca	tta	tta	ctg	gca	atg	aga	agt	aat	ggg	gaa	2448
Arg	Ile	Ala	Thr	Thr	Thr	Leu	Leu	Leu	Ala	Met	Arg	Ser	Asn	Gly	Glu	
				805					810					815		
gaa	gtg	aaa	gag	att	gga	atg	aaa	gct	att	gtg	gat	ata	ttg	gca	att	2496
Glu	Val	Lys	Glu	Ile	Gly	Met	Lys	Ala	Ile	Val	Asp	Ile	Leu	Ala	Ile	
			820					825					830			
tat	ggg	atg	agt	att	ctt	gat	aaa	tca	tct	aaa	tac	aaa	tat	tca	aga	2544
Tyr	Gly	Met	Ser	Ile	Leu	Asp	Lys	Ser	Ser	Lys	Tyr	Lys	Tyr	Ser	Arg	
		835					840					845				
atg	ttt	ttc	aaa	gtt	tta	aat	tca	ttt	gat	gca	cca	aaa	tta	caa	tgc	2592
Met	Phe	Phe	Lys	Val	Leu	Asn	Ser	Phe	Asp	Ala	Pro	Lys	Leu	Gln	Cys	
	850					855					860					
att	gtc	gct	gaa	gga	tta	tgc	aaa	ttg	ttt	tta	gcc	gat	att	ttg	tac	2640
Ile	Val	Ala	Glu	Gly	Leu	Cys	Lys	Leu	Phe	Leu	Ala	Asp	Ile	Leu	Tyr	

865	870	875	880	
aag act gac aaa cgg agt tta ttt gga aat gct att caa ggt ggt ggt				2688
Lys Thr Asp Lys Arg Ser Leu Phe Gly Asn Ala Ile Gln Gly Gly Gly	885	890	895	
ggt ggt ggt ggt ggt aat gat gat cca act acc acc aat gac gat gaa				2736
Gly Gly Gly Gly Gly Asn Asp Asp Pro Thr Thr Thr Asn Asp Asp Glu	900	905	910	
act gaa gaa gaa aca gat cga gag cat gaa aag cat tta ttt gaa gcg				2784
Thr Glu Glu Glu Thr Asp Arg Glu His Glu Lys His Leu Phe Glu Ala	915	920	925	
att gta ctt att tat ttc aac ccc aac acc aaa tca aat caa gaa tta				2832
Ile Val Leu Ile Tyr Phe Asn Pro Asn Thr Lys Ser Asn Gln Glu Leu	930	935	940	
caa caa att ttg tca ttt tgt att cca gtt tat gcc ttt tct cat ata				2880
Gln Gln Ile Leu Ser Phe Cys Ile Pro Val Tyr Ala Phe Ser His Ile	945	950	955	960
aat cat caa atc aat tta gct gca gtt agt ggt gat gtt att tat cga				2928
Asn His Gln Ile Asn Leu Ala Ala Val Ser Gly Asp Val Ile Tyr Arg	965	970	975	
ctt ttc act gaa aca gaa aca gaa tta tca cca agt gtt ata atc cct				2976
Leu Phe Thr Glu Thr Glu Thr Glu Leu Ser Pro Ser Val Ile Ile Pro	980	985	990	
caa tta ata tca tgg tgt gat cct cga aat tta gtt aaa tta tcg aat				3024
Gln Leu Ile Ser Trp Cys Asp Pro Arg Asn Leu Val Lys Leu Ser Asn	995	1000	1005	
gag gaa ata aat caa gca aca tca cat tta tgg caa tgt gtt tat tta				3072
Glu Glu Ile Asn Gln Ala Thr Ser His Leu Trp Gln Cys Val Tyr Leu	1010	1015	1020	
tta caa gtg gtt gaa caa gta gat gct cgt aat gtt aaa aga tgc atc				3120
Leu Gln Val Val Glu Gln Val Asp Ala Arg Asn Val Lys Arg Cys Ile	1025	1030	1035	1040
att aac aat ttg aat aaa ttt cat ata acg gaa gaa tta gag tca aat				3168
Ile Asn Asn Leu Asn Lys Phe His Ile Thr Glu Glu Leu Glu Ser Asn	1045	1050	1055	
caa tta caa gct tta att aaa gct ctt gat gct aca gtt gaa tta ttt				3216
Gln Leu Gln Ala Leu Ile Lys Ala Leu Asp Ala Thr Val Glu Leu Phe	1060	1065	1070	
act aat aat gaa gat aac cct aat ttt atc ttg gat aaa cca aca aag				3264
Thr Asn Asn Glu Asp Asn Pro Asn Phe Ile Leu Asp Lys Pro Thr Lys	1075	1080	1085	
aag aat ttt gat act ttt att gaa tca ata aag aat aaa ttg gaa att				3312
Lys Asn Phe Asp Thr Phe Ile Glu Ser Ile Lys Asn Lys Leu Glu Ile	1090	1095	1100	

gct caa aaa aga gaa gaa aat gaa ctg att aaa agt ggt aca aat tca 3360
 Ala Gln Lys Arg Glu Glu Asn Glu Leu Ile Lys Ser Gly Thr Asn Ser
 1105 1110 1115 1120
 ata tta cat gaa tta gat gat tta gat att gga act gga gag agt agt 3408
 Ile Leu His Glu Leu Asp Asp Leu Asp Ile Gly Thr Gly Glu Ser Ser
 1125 1130 1135
 caa ata tct ata aaa tca gaa aca aaa aga aga gat ctg gat cga tct 3456
 Gln Ile Ser Ile Lys Ser Glu Thr Lys Arg Arg Asp Leu Asp Arg Ser
 1140 1145 1150
 ctg caa gtt agt aaa act acg tca cca gaa act tca gaa aat gaa gat 3504
 Leu Gln Val Ser Lys Thr Thr Ser Pro Glu Thr Ser Glu Asn Glu Asp
 1155 1160 1165
 gaa gag gat gat aat gag gag gag gaa caa gag aag aag aaa agt ttt 3552
 Glu Glu Asp Asp Asn Glu Glu Glu Glu Gln Glu Lys Lys Lys Ser Phe
 1170 1175 1180
 act gat gga aaa aat aaa ctt gaa cta aag gca gat aag cca atc aca 3600
 Thr Asp Gly Lys Asn Lys Leu Glu Leu Lys Ala Asp Lys Pro Ile Thr
 1185 1190 1195 1200
 ttt aaa gct gaa gac aag agg gaa ggg tca gtt gaa aca gat cat ggt 3648
 Phe Lys Ala Glu Asp Lys Arg Glu Gly Ser Val Glu Thr Asp His Gly
 1205 1210 1215
 caa gaa caa gtt cta gtt gaa tca aag aaa gtc att gat agt aat gtt 3696
 Gln Glu Gln Val Leu Val Glu Ser Lys Lys Val Ile Asp Ser Asn Val
 1220 1225 1230
 gaa gat tct tta gaa gat ata gat aag ttt tta gaa gaa gca gat gat 3744
 Glu Asp Ser Leu Glu Asp Ile Asp Lys Phe Leu Glu Glu Ala Asp Asp
 1235 1240 1245
 gtt gat tat ggt gat att tca atg gat 3771
 Val Asp Tyr Gly Asp Ile Ser Met Asp
 1250 1255

<210> 21
 <211> 1257
 <212> PRT
 <213> Candida albicans

<400> 21
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 1 5 10 15
 Thr Leu Asp Glu Ile Lys Tyr Ala Met Lys His Val Phe Gln Asp Ala
 20 25 30
 Gln Leu Gly Leu Ala Gly His Arg Lys Leu Val Val Ile Leu Lys Asn
 35 40 45

Val Phe Lys Lys Ala Ile Glu Leu Asn Gln Ile Asn Phe Phe Ala Met
 50 55 60
 Cys Phe Thr Lys Leu Leu Ser Lys Val Leu Pro Leu Lys Arg Gly Val
 65 70 75 80
 Leu Ala Gly Asp Arg Ile Val Lys Phe Cys Tyr Leu Phe Val Asn Gly
 85 90 95
 Leu Val Lys Asp Ala Asn Glu Glu Lys Arg Ser Lys Glu Glu Glu Lys
 100 105 110
 Glu Glu Lys Asp Lys Asp Glu Asp Lys Asp Thr Asn Glu Ser Asp Lys
 115 120 125
 Asn Glu Glu Asp Gln Glu Asp Gln Glu Gly Glu Gly Asp Gln Glu Thr
 130 135 140
 Pro Ile Ser Glu Phe Ile Ser Tyr Leu Ile Lys Tyr Leu Leu Ser Gly
 145 150 155 160
 Ile Glu Ala Lys Asp Lys Leu Val Arg Tyr Arg Val Val Gln Thr Leu
 165 170 175
 Ala Tyr Leu Val Glu Phe Leu Thr Glu Ile His Glu Asn Asn Thr Leu
 180 185 190
 Glu Ala Leu Tyr Thr Leu Leu Ser Asn Arg Leu Gln Asp Lys Glu Leu
 195 200 205
 Ser Ile Arg Ile Gln Ala Val Val Ala Leu Ser His Phe Gln Leu Phe
 210 215 220
 Glu Phe Ser Ile Glu Gly Asp Thr Gly Glu Phe Glu Asp Glu Leu Ile
 225 230 235 240
 Ser Ser Asn Gln Ile Gln Asn Lys Leu Ile Asn Ser Ile Gln Asn Asp
 245 250 255
 Asp Ser Pro Glu Val Arg Arg Ala Ala Leu Met Asn Leu Val Lys Thr
 260 265 270
 Gln Asp Thr Ile Pro Ile Leu Leu Glu Arg Ala Arg Asp Ser Asn Ser
 275 280 285
 Ile Asn Arg Arg Leu Val Tyr Ser Lys Ile Ala Arg Glu Leu Ile Thr
 290 295 300
 Asp Leu Asp Asp Leu Glu Phe Glu Asp Arg Glu Phe Leu Leu Lys Trp
 305 310 315 320
 Gly Leu Asn Asp Arg Asp Glu Thr Val Lys Ala Ala Ala Thr Lys Met
 325 330 335
 Leu Thr Ile Tyr Trp Tyr Gln Ser Val Asn Glu Asp Leu Leu Glu Leu
 340 345 350

Ile Asp Gln Leu Asn Val Lys Ser Ala Ile Ala Glu Gln Ala Ile Leu
 355 360 365
 Ala Phe Phe Lys Asn Lys Pro Glu Val Leu Glu Thr Ile Lys Ile Asp
 370 375 380
 Glu Ser Tyr Trp Lys Asn Leu Thr Thr Glu Lys Ala Phe Leu Met Arg
 385 390 395 400
 Thr Phe Tyr Gln Tyr Cys Asn Glu Asn Gln Leu His Ala Leu Met Asp
 405 410 415
 Ala Asn Phe Pro Glu Leu Leu Asp Leu Ser Ile Thr Leu Glu Lys Tyr
 420 425 430
 Leu Ser Val Arg Leu Lys Thr Ile Asn Glu Asn Glu Asn Leu Val Lys
 435 440 445
 Thr Trp Glu Thr Tyr Asn Ala Lys Ile Asp Glu Leu Asp Asp Gln Ile
 450 455 460
 Phe Ser Leu Glu Asn Gln Ile Ser Arg Ile Asn Thr Asp Ala Asp Asn
 465 470 475 480
 Phe Arg Lys Ser Leu Ser Asn Ile Glu Glu Asp Ile Ile Glu Ile Asn
 485 490 495
 Ile Ala Lys Asp Leu Phe Lys Lys Arg Ile Lys Gln Leu Lys Asn Asn
 500 505 510
 Ser Gly Asn Leu Glu Asp Leu Ile Thr Glu Glu Asn Gln Glu Ile Ala
 515 520 525
 Asp Gln Ile Lys Asp Phe Leu Met Glu Asp Leu Gln Gln Gln Leu Glu
 530 535 540
 Asp Ile Asn Lys Asn Leu Asp Glu Ile Glu His His Pro Glu Asp Ile
 545 550 555 560
 Thr Ala Lys Leu Glu Glu Leu Gln Thr Lys Tyr Asp Ser Cys Ile Arg
 565 570 575
 Ala Leu Glu Thr Thr Ser Glu Leu Lys Ile Gln Thr Val Gln Ile Phe
 580 585 590
 Glu Gln Glu His Glu Asn Asp Cys Ile Pro Phe Val Asp Ala Leu Lys
 595 600 605
 Glu Leu Glu Phe Ile Ile Asn Gln Leu Leu Leu Ile Val Lys Asp Phe
 610 615 620
 Asp Tyr Gly Asp Glu Met Ala Arg Arg Lys Leu Leu His Ile Ile Arg
 625 630 635 640
 Met Thr Leu Thr Glu Asp Lys Leu Pro Asp Ala Leu Ile Ser Val Ala
 645 650 655

Leu Arg Val Leu Arg Ala Leu Ser Ile Asn Glu Lys Asp Phe Val Ser
 660 665 670
 Met Ala Val Glu Ile Ile Thr Asp Ile Arg Asp Ser Arg Asp Asp Glu
 675 680 685
 Glu Phe His Ser Ala Ala Ala Thr Phe Asp Asp Asp Asp Asp Ile
 690 695 700
 Leu Gly Asn Gly Asp Asp Glu Ser Gln Gln Ser Ser Ser Leu Ser Ala
 705 710 715 720
 Val Thr Lys Lys Arg Arg Ile Glu Pro Asp Met Pro Pro Asp Asp Ile
 725 730 735
 Val Leu Arg Cys Leu Thr Met Thr Gln Tyr Val Leu Glu Val Ile Thr
 740 745 750
 His Ser Leu Asp Asp His Leu Ser Leu Ser Ser Ile Tyr Ser Gly Ile
 755 760 765
 Val Asn Tyr Ala Ile Gln Asn Glu Ser Lys Lys Lys Leu Tyr Leu Ala
 770 775 780
 Gly Leu Thr Cys Leu Gly Leu Tyr Ser Leu Ile Asp Ser Lys Ile Ala
 785 790 795 800
 Arg Ile Ala Thr Thr Thr Leu Leu Leu Ala Met Arg Ser Asn Gly Glu
 805 810 815
 Glu Val Lys Glu Ile Gly Met Lys Ala Ile Val Asp Ile Leu Ala Ile
 820 825 830
 Tyr Gly Met Ser Ile Leu Asp Lys Ser Ser Lys Tyr Lys Tyr Ser Arg
 835 840 845
 Met Phe Phe Lys Val Leu Asn Ser Phe Asp Ala Pro Lys Leu Gln Cys
 850 855 860
 Ile Val Ala Glu Gly Leu Cys Lys Leu Phe Leu Ala Asp Ile Leu Tyr
 865 870 875 880
 Lys Thr Asp Lys Arg Ser Leu Phe Gly Asn Ala Ile Gln Gly Gly Gly
 885 890 895
 Gly Gly Gly Gly Gly Asn Asp Asp Pro Thr Thr Thr Asn Asp Asp Glu
 900 905 910
 Thr Glu Glu Glu Thr Asp Arg Glu His Glu Lys His Leu Phe Glu Ala
 915 920 925
 Ile Val Leu Ile Tyr Phe Asn Pro Asn Thr Lys Ser Asn Gln Glu Leu
 930 935 940
 Gln Gln Ile Leu Ser Phe Cys Ile Pro Val Tyr Ala Phe Ser His Ile
 945 950 955 960

Asn His Gln Ile Asn Leu Ala Ala Val Ser Gly Asp Val Ile Tyr Arg
 965 970 975
 Leu Phe Thr Glu Thr Glu Thr Glu Leu Ser Pro Ser Val Ile Ile Pro
 980 985 990
 Gln Leu Ile Ser Trp Cys Asp Pro Arg Asn Leu Val Lys Leu Ser Asn
 995 1000 1005
 Glu Glu Ile Asn Gln Ala Thr Ser His Leu Trp Gln Cys Val Tyr Leu
 1010 1015 1020
 Leu Gln Val Val Glu Gln Val Asp Ala Arg Asn Val Lys Arg Cys Ile
 1025 1030 1035 1040
 Ile Asn Asn Leu Asn Lys Phe His Ile Thr Glu Glu Leu Glu Ser Asn
 1045 1050 1055
 Gln Leu Gln Ala Leu Ile Lys Ala Leu Asp Ala Thr Val Glu Leu Phe
 1060 1065 1070
 Thr Asn Asn Glu Asp Asn Pro Asn Phe Ile Leu Asp Lys Pro Thr Lys
 1075 1080 1085
 Lys Asn Phe Asp Thr Phe Ile Glu Ser Ile Lys Asn Lys Leu Glu Ile
 1090 1095 1100
 Ala Gln Lys Arg Glu Glu Asn Glu Leu Ile Lys Ser Gly Thr Asn Ser
 1105 1110 1115 1120
 Ile Leu His Glu Leu Asp Asp Leu Asp Ile Gly Thr Gly Glu Ser Ser
 1125 1130 1135
 Gln Ile Ser Ile Lys Ser Glu Thr Lys Arg Arg Asp Leu Asp Arg Ser
 1140 1145 1150
 Leu Gln Val Ser Lys Thr Thr Ser Pro Glu Thr Ser Glu Asn Glu Asp
 1155 1160 1165
 Glu Glu Asp Asp Asn Glu Glu Glu Glu Gln Glu Lys Lys Lys Ser Phe
 1170 1175 1180
 Thr Asp Gly Lys Asn Lys Leu Glu Leu Lys Ala Asp Lys Pro Ile Thr
 1185 1190 1195 1200
 Phe Lys Ala Glu Asp Lys Arg Glu Gly Ser Val Glu Thr Asp His Gly
 1205 1210 1215
 Gln Glu Gln Val Leu Val Glu Ser Lys Lys Val Ile Asp Ser Asn Val
 1220 1225 1230
 Glu Asp Ser Leu Glu Asp Ile Asp Lys Phe Leu Glu Glu Ala Asp Asp
 1235 1240 1245
 Val Asp Tyr Gly Asp Ile Ser Met Asp
 1250 1255

<210> 22
 <211> 603
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Homologous
 Fragment to Sc YDR325

<400> 22

ctgtttgtta atggtcttgt aaaagatgcc aatgaagaaa aacgttccaa agaagaagaa 60
 aaagaagaga aagacaaaga caaagacaaa gatacgaatg aaagtgataa aaatgaagaa 120
 gatcaggaag atcaagaagg agaaggagat caagaaactc caatttcgga attcatatca 180
 tatttgataa aatattttatt gagtgggata gaggctaaag ataaactggg tcgttatcgt 240
 gttgtacaaa cattagcata cttgggttgaa ttcttgaccg agatacacga gaataatata 300
 ttggaagcgt tatatacttt attaagtaat aggcatacag ataaagagct gtcgatacgt 360
 attcaagctg ttgtggcatt atcacatttt caattatttg aatttagtat tgaaggtgat 420
 actggagaat ttgaggatga attaatatca agtaacccaa ttcagaataa attgataaat 480
 tccattcaaa atgatgatag tccagaagtc agacgtgcag cattaatgaa tttgggttaa 540
 acacaagata caataccgat ttacttgag cgagccagag attccaattc tattaataga 600
 aga 603

<210> 23
 <211> 581
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Homologous
 Fragment to Sc YDR325

<400> 23

ggggttaaat gatcgtgatg aatctgttaa agcagccgcc tttaaaatgc taaccattta 60
 ttggtatcaa tctgtcaatg aagattttatt agaattaatt gatcaattaa atgtcagaag 120
 tgctatagct gaacaggcca tattagcatt ttttaaaaat aaaccagaag ttcttgcaac 180
 tattaaaatt gatgaatcat attggaaaaa tctaactaca gaaaaggcat tcttgatgag 240
 gacgttttat caatattgta atgagaatca attacatgct ttaatggatg ccaatttccc 300
 tgaattactt gatttgtcaa taacattaga aaagtatttg tcagtggagt tgaaaacaat 360
 aatgaaaat gaaaatttaa ttaagacatg ggaaacttat aatgccaaga ttgacgaatt 420

agatgatcaa atatttagtc ttgaaaacca gatttccaga ataaatactg atgccgataa 480
 ttcccgtaaa agtttatcta acattgaaga agatattatt gaaatcaata ttgctaagga 540
 ttgtttcaaa aagagaatta aacaattgaa aaactgagca c 581

<210> 24

<211> 662

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Homologous
 Fragment to Sc YDR325

<400> 24

tggtgactca attcatttga tgcacaaaaa ttacaatgca ttgtcgctga gtagattatg 60
 caaattgttt ttagccgata ttttgtacaa gactgacaaa cggatttatt tggaaatgct 120
 attcaagggtg gtggtggtgg tgatgatcca actaccacca atgacgatga aactgaagaa 180
 gaaacagatc gagagcatga aaagcattta tttgaagcga ttgtacttat ttatttcaac 240
 cccaacacca aatcaaatac agaattacaa caaattttgt cattttgtat tccagtttat 300
 gcctttttctc atataaatca tcaaatcaat ttagctgcag ttagtggtga tgttatttat 360
 cgacttttca ctgaaacaga aacagaatta tcaccaagtg ttataatccc tcaattaata 420
 tcatggtgtg atcctcgaaa tttagttaaa ttatcgaatg aggaaataaa tcaagcaaca 480
 tcacatttat ggcaatgtgt ttatttatta caagtgggtg aacaagtaga tgctcgtaat 540
 gttaaaagat gcatcattaa caatttgaat aaatttcata taacggaaga attagaatca 600
 aatcaattac aagctttaat taaagctctt gatgctacag ttgaattatt tactaataat 660
 ga 662

<210> 25

<211> 231

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Homologous
 Fragment to Sc YOR110

<400> 25

atatgtgttg atagttacac atgcagcaac gaaaattgct ttaggatcag ctttattaca 60
 gttaaaatca gttactgatg ttatagatga taatcaaact gtgttacgtg ctggtgcatg 120

ttcattatcc aaatttggtta gagatggcga agataaaacc aatcatacta ttcaatggaa 180

aattgtcatg aatggtaatt gtgaattctt gacacaggggt gaagaaatga a 231

aaa gag att gga atg aaa gct att gtg gat ata ttg gca att 2496
 Glu Val Lys Glu Ile Gly Met Lys Ala Ile Val Asp Ile Leu Ala Ile
 820 825 830

tat ggt atg agt att ctt gat aaa tca tct aaa tac aaa tat tca aga 2544
 Tyr Gly Met Ser Ile Leu Asp Lys Ser Ser Lys Tyr Lys Tyr Ser Arg
 835 840 845

atg ttt ttc aaa gtt tta aat tca ttt gat gca cca aaa tta caa tgc 2592
 Met Phe Phe Lys Val Leu Asn Ser Phe Asp Ala Pro Lys Leu Gln Cys
 850 855 860

att gtc gct gaa gga tta tgc aaa ttg ttt tta gcc gat att ttg tac 2640
 Ile Val Ala Glu Gly Leu Cys Lys Leu Phe Leu Ala Asp Ile Leu Tyr
 865 870 875 880

aag act gac aaa cgg agt tta ttt gga aat gct att caa ggt ggt ggt 2688
 Lys Thr Asp Lys Arg Ser Leu Phe Gly Asn Ala Ile Gln Gly Gly Gly
 885 890 895

ggg ggt ggt ggt ggt aat gat gat cca act acc acc aat gac gat gaa 2736
 Gly Gly Gly Gly Gly Asn Asp Asp Pro Thr Thr Thr Asn Asp Asp Glu
 900 905 910

act gaa gaa gaa aca gat cga gag cat gaa aag cat tta ttt gaa gcg 2784
 Thr Glu Glu Glu Thr Asp Arg Glu His Glu Lys His Leu Phe Glu Ala
 915 920 925

att gta ctt att tat ttc aac ccc aac acc aaa tca aat caa gaa tta 2832
 Ile Val Leu Ile Tyr Phe Asn Pro Asn Thr Lys Ser Asn Gln Glu Leu
 930 935 940

caa caa att ttg tca ttt tgt att cca gtt tat gcc ttt tct cat ata 2880
 Gln Gln Ile Leu Ser Phe Cys Ile Pro Val Tyr Ala Phe Ser His Ile
 945 950 955 960

aat cat caa atc aat tta gct gca gtt agt ggt gat gtt att tat cga 2928
 Asn His Gln Ile Asn Leu Ala Ala Val Ser Gly Asp Val Ile Tyr Arg
 965 970 975

ctt ttc act gaa aca gaa aca gaa tta tca cca agt gtt ata atc cct 2976
 Leu Phe Thr Glu Thr Glu Thr Glu Leu Ser Pro Ser Val Ile Ile Pro
 980 985 990

caa tta ata tca tgg tgt gat cct cga aat tta gtt aaa tta tcg aat 3024
 Gln Leu Ile Ser Trp Cys Asp Pro Arg Asn Leu Val Lys Leu Ser Asn
 995 1000 1005

gag gaa ata aat caa gca aca tca cat tta tgg caa tgt gtt tat tta 3072
 Glu Glu Ile Asn Gln Ala Thr Ser His Leu Trp Gln Cys Val Tyr Leu
 1010 1015 1020

tta caa gtg gtt gaa caa gta gat gct cgt aat gtt aaa aga tgc atc 3120
Leu Gln Val Val Glu Gln Val Asp Ala Arg Asn Val Lys Arg Cys Ile
1025 1030 1035 1040

att aac aat ttg a